

STIC-Biotech/ChemLib

From: Whiteman, Brian
Sent: Monday, April 28, 2003 10:43 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09/818,943 3/28/01
Eriksson et al.

search seq id nos: 1 and 2 against us patent and us patent application databases.

Claiming a transgenic mouse comprising a nucleotide encoding either seq id no: 1 or 2.

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Point of Contact:
Toby Port
Technical Info. Specialist
CRM1 6A04
703-302-2534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/29
Date Completed: 4/29
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:36 ; Search time 12.5 Seconds

(Without alignments)
812.073 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
Sequence: 1 MSLEGLLVTSALAGORGT.....DVALEHHECDVCVGSTGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/CTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
2	1851	99.6	345	US-09-457-066-2	Sequence 2, Appl
3	1851	99.6	345	US-09-265-686-2	Sequence 2, Appl
4	1851	99.6	345	US-09-540-224-5	Sequence 5, Appl
5	1664	89.6	345	US-09-457-066-43	Sequence 43, Appl
6	741.5	39.9	370	US-09-457-066-37	Sequence 37, Appl
7	741.5	39.9	370	US-09-540-224-2	Sequence 2, Appl
8	737.5	39.7	370	US-09-540-224-4	Sequence 4, Appl
9	172.5	9.3	730	US-08-872-757-2	Sequence 2, Appl
10	169	9.1	788	US-08-572-225-1	Sequence 1, Appl
11	164.5	8.9	906	US-08-936-135-18	Sequence 18, Appl
12	164.5	8.9	906	US-08-936-135-20	Sequence 20, Appl
13	163.5	8.8	922	US-09-116-473-4	Sequence 4, Appl
14	163	8.8	101	US-09-374-135-6	Sequence 6, Appl
15	160.5	8.6	925	US-09-116-473-2	Sequence 2, Appl
16	160.5	8.6	906	US-08-936-135-22	Sequence 22, Appl
17	160.5	8.6	906	US-08-936-135-24	Sequence 24, Appl
18	160.5	8.6	909	US-08-936-135-8	Sequence 8, Appl
19	160.5	8.6	909	US-08-936-135-10	Sequence 10, Appl
20	160.5	8.6	914	US-08-936-135-12	Sequence 12, Appl
21	160.5	8.6	923	US-08-936-135-6	Sequence 6, Appl
22	160.5	8.6	926	US-08-936-135-14	Sequence 14, Appl
23	160.5	8.6	931	US-08-936-135-16	Sequence 16, Appl
24	156	8.4	986	US-08-872-757-4	Sequence 4, Appl
25	154	8.3	449	US-08-839-008-2	Sequence 2, Appl
26	154	8.3	449	US-08-839-008-9	Sequence 9, Appl
27	153	8.2	415	US-09-032-523-2	Sequence 2, Appl

28	149	8.0	591	US-08-991-408-4	Sequence 4, Appl
29	149	8.0	591	US-09-432-473-4	Sequence 4, Appl
30	149	8.0	1013	US-08-866-650-5	Sequence 5, Appl
31	149	8.0	1013	US-09-021-287-5	Sequence 5, Appl
32	149	8.0	1013	US-08-991-408-2	Sequence 2, Appl
33	149	8.0	1013	US-09-240-473-5	Sequence 5, Appl
34	149	8.0	1013	US-09-432-473-2	Sequence 2, Appl
35	148	8.0	1013	US-08-866-650-3	Sequence 3, Appl
36	148	8.0	1013	US-09-021-287-3	Sequence 3, Appl
37	148	8.0	1013	US-09-240-473-3	Sequence 3, Appl
38	147	7.9	354	US-08-915-795-5	Sequence 5, Appl
39	142	7.6	325	US-08-915-795-3	Sequence 3, Appl
40	140	7.5	103	US-09-374-135-5	Sequence 5, Appl
41	140	7.5	321	US-08-915-795-9	Sequence 9, Appl
42	140	7.5	358	US-08-915-795-8	Sequence 8, Appl
43	132	7.1	95	US-09-374-135-8	Sequence 8, Appl
44	132	7.1	419	US-08-999-811-2	Sequence 2, Appl
45	132	7.1	419	US-09-042-105-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-040-220D-2
; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match 99.6% Score 1851; DB 4; Length 345;
Best Local Similarity 99.4% Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLVTSALAGORGTGAESNLSKRFQESSNKEONGVODPQHERIITVSTNGSIHS 60
DB 1 MSLEGLLVTSALAGORGTGAESNLSKRFQESSNKEONGVODPQHERIITVSTNGSIHS 60
QY 61 PREPHYPRNTVLMVRLVAEEVNMVQLTFDERFGLDEPDDICKYFVEVEEPSDGTLL 120
DB 61 PREPHYPRNTVLMVRLVAEEVNMVQLTFDERFGLDEPDDICKYFVEVEEPSDGTLL 120
QY 121 GRWCGGTVPGRKISGNQRIREFVDEFPSPGCIHYNTVMPQFTAVSVLPSPA 180
DB 121 GRWCGGTVPGRKISGNQRIREFVDEFPSPGCIHYNTVMPQFTAVSVLPSPA 180
QY 181 LPDLNNAITASTEDLIRYLEPERMOLDLRLPTMOLGKAFVGRKSRVVDLNL 240
DB 181 LPDLNNAITASTEDLIRYLEPERMOLDLRLPTMOLGKAFVGRKSRVVDLNL 240
QY 241 LREEVRLVYCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGACACCLHNCNCCQVPSK 300
DB 241 LREEVRLVYCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGACACCLHNCNCCQVPSK 300
QY 301 VTKKYEIVLQRPKTVGRGLHKSITDVALEHHECDVCVGSTGG 345
DB 301 VTKKYEIVLQRPKTVGRGLHKSITDVALEHHECDVCVGSTGG 345

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RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match          99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSFGLLVTSALAGORGTQAESNLSSKFOFSSNKQNGVDPQHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
DB 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LPEEVRLYSCTPRNFVSYSIREELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
DB 241 LPEEVRLYSCTPRNFVSYSIREELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
QY 301 VTKKYEVLQLRPKTGVGRLHKSITDVALEHHECDVCVCGSTGG 345
DB 301 VTKKYEVLQLRPKTGVGRLHKSITDVALEHHECDVCVCGSTGG 345

RESULT 3
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
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US-09-265-686-2

Query Match          99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSFGLLVTSALAGORGTQAESNLSSKFOFSSNKQNGVDPQHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
DB 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LPEEVRLYSCTPRNFVSYSIREELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
DB 241 LPEEVRLYSCTPRNFVSYSIREELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
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DB 301 VTKKYEVLQLRPKTGVGRLHKSITDVALEHHECDVCVCGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match          99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSFGLLVTSALAGORGTQAESNLSSKFOFSSNKQNGVDPQHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
DB 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQFTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLGKAFVGRKSRVVDNL 240
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Db      5 IFVYTTICANFCCSCRDTSATPOSASIKALRNANLRDESNHLLDLYKRDETIQVKGNGYV 64
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Db      65 QSPRFPNTPRNLLTWRLHS--QENTRIQLVFNQGLAEANDICRYDVEVEEDSETS 123
QY      119 --ILGRWCGSGTVPKQKISKNOIRIRFVDEFEPSGFCIHYNIMPOFTEAV----- 171
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      124 TIRGRMCGHKEVPRIKSTNOIKTFKSDDFVAKPGKITYSL--LEDFQANASETN 182
QY      172 -----SPSVLPSPALPLDLNNAITAESTDILIRYLEPERWOLDEDLYR 217
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      183 WESVTSISGSVSNPSVTDPT--LIADALDKIAEFDVYEDLKTFEPMOEDLEMYL 241
QY      218 PTWOLLGKAFVFGKSGVVDVNLTFEVRYSCTPRNFVSIRBELKRTDTIMPGLLV 277
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Db      242 DTPRYRKRSY-HDRKSK-VLDLRINDAKRYSCTPRNYSVINEELKLAVVEPRCLLV 299
QY      278 KRCGNCACCLHNCNECQVPSKYTKKHYEVLQLRP---KTGVGRLHKSITDVALEHHEE 334
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      300 QRCGNCGGCTVMWRSCOTCNSGKTAKHYEVLQFEFGHIRRGRAKTMALVDIQLDHER 359
QY      335 CDCVC 339
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RESULT 8
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGR4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; EARLIER FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

Query Match          39.7%; Score 737.5; DB 4; Length 370;
Best Local Similarity 44.0%; Pred. No. 8.4e-72;
Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;

QY      16 QRRGTAESNLSSKFOFSSNKEONGYOD--POHRIITVSTNGSIHSPRPHTYRNATLV 74
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Db      26 QRASIKALRNANLR-----RDESNHLLDLYQRENIQVTSNGHQSPRNFNSPRNLLT 80
QY      75 WRVLAIVENWIOITFDERGLEDPEDDICKYFVEVEEESDGT--ILGRWCGSGTVPK 132
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Db      81 WMLRS--QEKTRIQLSPDHQGLEAENDICRYDVEVEEVEESSVYVGRWCGHKEIPR 139
QY      133 QISKNOIRIRFVDEFEPSGFCIHYNIMVMOFTEAV-----SPS 174
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      140 ITRTNOIKTFESDDFTVAKPGKITYSEVEDPOPEASETWESVTSFSGVSYHSPS 199
QY      175 VLPSPALPLDLNNAITAESTDILIRYLEPERWOLDEDLYRPTWOLLGKAFVFGKRSR 234
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Db      200 ITDPT--LTADALDKIAEFDVYEDLKTFEPMOEDLEMYLDTDTPHYRKRSY-HDRKSK 257
QY      235 VVDLNLTFEVRYSCTPRNFVSIRBELKRTDTIMPGLLVKRCGNCACCLHNCNEC 294
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      258 -VLDLRINDVKKRYSCPTPRNHSYVNLREELKLTAVFFPRCLLVQRCGNCGGCTVMWKS 316
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QY      295 QCVPSKYTKKHYEVLQLRP---KTGVGRLHKSITDVALEHHEECDCVC 339
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Db      317 TCSSGKTAKHYEVLQFEFGHFRGRGAKNMALVDIQLDHERDCIC 364

RESULT 9
US-08-872-757-2
; Sequence 2, Application US/08872757
; Patent No. 6258564
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Alexander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,757
; FILING DATE: 10-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,187
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-757-2

Query Match          9.3%; Score 172.5; DB 4; Length 730;
Best Local Similarity 36.6%; Pred. No. 7.3e-10;
Matches 49; Conservative 20; Mismatches 48; Indels 17; Gaps 7;

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Db      599 NGISITSGWKEVPPKNCIMOLVAPYRISLQFFETEG-----NDVCKYDFVEVRS 653
QY      114 --PSDGTILGRWCGSGTVPKQKISKNOIRIRFVDEFEPSGFCIHYNIMVMOFTEAV 171
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      654 GLTAHSLKHGKFCGS--EKPEVITISQINNMVRFKSDNTV--SKGGRANF-----FSEN 704
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      172 SPSVLPSPALPLDL 185
        |||||:
Db      705 RPALQPPRGPQHOL 718

RESULT 10
US-08-572-225-1
; Sequence 1, Application US/08572225
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; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halliuid, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-572-225-1
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Query Match          9.1%; Score 169; DB 1; Length 788;
Best Local Similarity 39.4%; Pred. No. 2e-09;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 55 NSGHSRPHPTVPRNTVLVRLVA-VEENWVQLTFDERFGLEDPEDDICKYDFVEVEE 113
    |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 401 NSGTSHPGMKEYPNKNCIMQLVAPLQYRIISQDFEFETEG-----NDVCXTDFVEVRS 455

QY 114 --PSDGTILGRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEFGFCHY 160
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 456 GLTADSKLMGKFCGS-EKPEVITSQYNMNRKESDNTV-SKKGFAHF 502
```

```
RESULT 11
US-08-936-135-18
; Sequence 18, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-18
```

```
Query Match          8.9%; Score 164.5; DB 3; Length 909;
Best Local Similarity 29.9%; Pred. No. 7.5e-09;
Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;

QY 1 MSLEGLLVTSALAGORGTQAESNLSSKRFSSNKQNGVQDPQHRILITVSTNGSIHS 60
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 1 MDMEPLTWVFLA-----YSRHQVRGQPPPPCGGRINMSKDAQYIIS 42

QY 61 PRPHPTVPRNTVLVRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEVE--EPSDGT 118
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 43 PGYPDYPSSHQNCWIVYVPEPNQKTVLNFNPHFEIEKHD---CKYDFLEIRGDSESD 99

QY 119 ILGRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEFGFCHYNI 162
    |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 100 LLSRMCGN-IAPPTIISGSMLYIKFTSD-YANQAGAFSLRYEI 141
```

```
RESULT 12
US-08-936-135-20
; Sequence 20, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
```


APPLICATION NUMBER: US/09/116,473
FILING DATE: 17-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/052,762
FILING DATE: 17-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.74973
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-116-473-2

Query Match 8.8%; Score 163; DB 4; Length 925;
Best Local Similarity 33.8%; Pred. No. 1.1e-08;
Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;
QY 32 FSNKKEONGVODQHRIITVSTNGSIHSRPPHTYPRNTVLWRLVAVEENWIOLEFD 91
DB 15 FSGHKVRS-QQDPCCGRKNSKDAGYITSPGYQDIPSHONCEWVYAPENOKIVLNFN 73
QY 92 ERGLDEPDEDICKYDVEVE--EPSDGTILGRWCGSGTVPGKQISKGNQIRIFVSDEY 149
DB 74 PHEIEIKHD--CKYDPIELROGDSSESADLLGKHGCM-INPILISGSVLYIKFTSD-Y 128
QY 150 FSEPGFCIHNT 162
DB 129 AROGAGFSLRYEI 141

Search completed: April 29, 2003, 09:09:16
Job time : 15.5 secs

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xx	Eriksson U, Aase K, Lee X, Porten A, Untela M, Aitalo K;
pi	Oestman A, Heidln C, Betsholz C;
xx	WPI: 2000-292954/25.
DR	N-PSDB; AAA12523.
xx	
PT	Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT	differentiation, growth and motility of cells expressing the PDGF-C
PT	receptor
xx	
PS	Claim 27; Fig 2; 135pp; English.
xx	
CC	The present sequence represents human platelet-derived growth factor C
CC	(PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
CC	ability to stimulate and enhance proliferation or differentiation,
CC	and/or growth or motility of cells expressing a PDGF-C receptor.
CC	PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC	proliferation, preferably in combination with one other growth factor
CC	and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC	be used for stimulating connective tissue or wound healing. The
CC	PDGF-C polypeptide can be enzymatically processed to generate the active
CC	truncated form of PDGF-C and used to regulate the receptor-binding
CC	specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC	mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC	PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC	expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC	choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC	and erythroleukemia, can be identified by testing for expression of
CC	PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC	remodelling during invasion of tumour cells into a normal population of
CC	cells. Antagonists can also be used to treat fibrotic conditions,
CC	especially found in the lung, kidney or liver.
xx	
50	Sequence 345 AA:
Query Match	100.0%; Score 1858; DB 21; Length 345;
Best Local Similarity	100.0%; Pred. No. 1.7e-179;
Matches 345; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MSFLGLLVTSLAGORRGTQAESNLSSKFPSSKNKQGVODPOHERITITVSTNGSIHS 60
DB	1 MSFLGLLVTSLAGORRGTQAESNLSSKFPSSKNKQGVODPOHERITITVSTNGSIHS 60
OY	61 PREPHTYPRNTLVWRLVAEENVAIQLTFDRFGLEDPEDDICKYDYVEEPESDGTL 120
DB	61 PREPHTYPRNTLVWRLVAEENVAIQLTFDRFGLEDPEDDICKYDYVEEPESDGTL 120
OY	121 GWCSCSGTYPGKQISKGNQIRIRFVSDEFPSEPGFCHYNTVMQFTEAVSPSLPSPA 180
DB	121 GWCSCSGTYPGKQISKGNQIRIRFVSDEFPSEPGFCHYNTVMQFTEAVSPSLPSPA 180
OY	181 LPDLNLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
DB	181 LPDLNLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
OY	241 LEEEVRLVSCPRNRSVSIARELKTPTDTFMFGCLLYKRGCGNACCLHNCNECCVPSK 300
DB	241 LEEEVRLVSCPRNRSVSIARELKTPTDTFMFGCLLYKRGCGNACCLHNCNECCVPSK 300
OY	301 VTKKTHEVLDLPRKTGVRLHKSLLDVALLEHNEECDCVCRSGTGG 345
DB	301 VTKKTHEVLDLPRKTGVRLHKSLLDVALLEHNEECDCVCRSGTGG 345
RESULT 2	
AAEI3212	
XX	AAEI3212 standard; Protein: 345 AA.
XX	AAEI3212;
XX	
DT	12-FEB-2002 (first entry)
XX	

DE Human platelet-derived growth factor (PDGF-C) protein.
XX
XX Human; transgenic animal; platelet derived growth factor C; PDGF-C;
KW cardiac hypertrophy; fibrosis.
XX
XX Homo sapiens.
OS
WO200172132-A1.
PN
PD 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09855.
PF
XX 28-MAR-2000; 2000US-192507P.
ER
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Eriksson U, Li X, Ponten A, Aase K, Li H;
PI
DR WPI: 2002-010700/01.
XX
XX
PT A transgenic animal over-expressing platelet derived growth factor C is
PT useful to study and find therapy for disease associated with PDGF-C
PT over-expression, including cardiac hypertrophy and fibrosis
PS
XX Disclosure: Page 40-42; 48pp; English.
XX
XX The patent discloses a method for producing a transgenic, non-human
CC animal over-expressing a platelet derived growth factor C (PDGF-C),
CC or its functional fragment or analogue. The method involves introducing
CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing
CC the cell into a non-human animal and allowing the cell to develop into
CC a transgenic, non-human animal. The transgenic animal is useful as a
CC model to study disease states characterised by over-expression of PDGF-C
CC and to find therapy for those diseases, particularly hypertrophy and
CC fibrosis in various organs including the heart. The present sequence
CC is PDGF-C protein from human.
XX
XX Sequence 345 AA;
XX

Query Match	100.0%	Score 1858:	DB 23:	Length 345:
Best Local Similarity	100.0%	Pred. No. 1.7e-179:		
Matches 345:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0
QY 1	MSFLGLLVTSALAGORRGTOAESNLSSKFPQSSNKQNGVODPOHERLITVSTNGSIHS	60		
Db 1	MSFLGLLVTSALAGORRGTOAESNLSSKFPQSSNKQNGVODPOHERLITVSTNGSIHS	60		
QY 61	PRFPTTYRNMYLVRIAVAEENWMIQLTFDERFGLEDEEDDICKYDFEVEEPPSGTLL	120		
Db 61	PRFPTTYRNMYLVRIAVAEENWMIQLTFDERFGLEDEEDDICKYDFEVEEPPSGTLL	120		
QY 121	GRMGSGTVPGKQISKGNQIRIRFVSDSEYFPEPSPGCIHYNIIVMPQFTFAVSPSLPSPA	180		
Db 121	GRMGSGTVPGKQISKGNQIRIRFVSDSEYFPEPSPGCIHYNIIVMPQFTFAVSPSLPSPA	180		
QY 181	LPDLLNNAITAFSTLEDLIRLPEERPMQDLIEDLYRPTMOLLGKAIFYGGRKSRVYDLM	240		
Db 181	LPDLLNNAITAFSTLEDLIRLPEERPMQDLIEDLYRPTMOLLGKAIFYGGRKSRVYDLM	240		
QY 241	LTEEVRLEYSCPTPRNRSVSIIREELKRTDTIRFWMGCLLVKRGCGNCAQCLINCNCEOCVPSK	300		
Db 241	LTEEVRLEYSCPTPRNRSVSIIREELKRTDTIRFWMGCLLVKRGCGNCAQCLINCNCEOCVPSK	300		
QY 301	VTKKYHEVLQLRPKTGVGRGLHKSITLDAVALEHHHECCDCYCRSGSTGG	345		
Db 301	VTKKYHEVLQLRPKTGVGRGLHKSITLDAVALEHHHECCDCYCRSGSTGG	345		

RESULT 3
 AAY33679
 ID AAY33679 standard: Protein: 345 AA.

AC AAY33679;
XX
DT 11-JAN-2000 (first entry)
XX
DE Human VEGF-E protein.
XX
KM VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KM treatment; cardiovascular disorder; endothelial disorder; therapy;
KM tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KM angiogenic disorder; age-related macular degeneration; vascular disease;
KM neovascularization; tumor; gene mapping.
XX
OS Homo sapiens.
PN MO9947677-A2.
XX
PD 23-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US05190.
XX
PR 17-MAR-1998; 98US-0040220.
PR 02-NOV-1998; 98US-0184216.
XX
PA (GETH) GENENTECH INC.
PI Ferrara N, Kuo SS;
DR MPI; 1999-580306/49.
DR N-PSDB; AA223691.
XX
PT New growth factor polypeptide useful for treating cardiovascular or
XX endothelial disorders, e.g. cardiac hypertrophy
XX
XX Claim 1; Fig 2; 122pp; English.
XX
CC This invention describes the isolation of a novel human vascular
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
CC tranquillizer, vulnery and cardiant activity. VEGF-E can be administered
CC therapeutically, especially by expressing encoding polynucleotides, to
CC treat cardiovascular or endothelial disorders in mammals, especially
CC humans. It is useful in wound repair and tissue generation and
CC regeneration, and may especially be used to treat cardiac hypertrophy
CC It can be combined with a carrier in pharmaceutical compositions, which
CC can be administered to treat disorders as above. VEGF-E can be used to
CC screen for antagonists and agonists, and the antagonists administered to
CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
CC age-related macular degeneration. It can be used to generate antibodies,
CC useful therapeutically as antagonists, as above. The antibodies are also
CC useful to detect VEGF-E polypeptide, especially to diagnose
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
CC by contacting the antibody with a tissue sample and detecting formation
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
CC tissue samples. They can also be used to diagnose a disease or
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
CC sample. They may also be used to produce probes useful to detect related
CC sequences or for gene mapping. This sequence represents the human VEGF-E
CC protein described in the method of the invention.
XX
XX Sequence 345 AA:
SQ

Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLTVSALAGRGTOAESNLRSKFQSSNKEQNGVDPQHERITVSTNGSIHS 60
DB 1 MSIFGLLTVSALAGRGTOAESNLRSKFQSSNKEQNGVDPQHERITVSTNGSIHS 60

QY 61 PREPHYTPRNTVLVWRLVAEENWVITQLTFDERFGLDEPEDDICKYDFVEVEPSDGTLL 120
DB 61 PREPHYTPRNTVLVWRLVAEENWVITQLTFDERFGLDEPEDDICKYDFVEVEPSDGTLL 120
QY 121 GRWCGSGTVPGKOISKGNQIRIFVSDVFPSPGCIHYNIVMPQFTEAVSPSVLPSSA 180
DB 121 GRWCGSGTVPGKOISKGNQIRIFVSDVFPSPGCIHYNIVMPQFTEAVSPSVLPSSA 180
QY 181 LPDDLNNATTAATSTEDLIRYLEPFRWMDLFDLTPMQLGKAFVGRKSRVVDLNN 240
DB 181 LPDDLNNATTAATSTEDLIRYLEPFRWMDLFDLTPMQLGKAFVGRKSRVVDLNN 240
QY 241 LTEEVRLYSCTPRNFVSYSIREELKRTDTLFWPGCLLVKRCGNCACCLHNCNCCVPSK 300
DB 241 LTEEVRLYSCTPRNFVSYSIREELKRTDTLFWPGCLLVKRCGNCACCLHNCNCCVPSK 300
QY 301 VTKKHYEVILQRPKTVGRGLKSLTDVALLHEHECCVCVCGSTGG 345
DB 301 VTKKHYEVILQRPKTVGRGLKSLTDVALLHEHECCVCVCGSTGG 345

RESULT 4
ID AAY41766
AA41766
XX AAY41766 standard; Protein; 345 AA.
AC AAY41766;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO200 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
XX Homo sapiens.
OS
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.

PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081932.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI
XX WPI; 1999-551358/46.
DR N-PSDB; AA234296.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 12; Fig 207; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC

CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX Sequence 345 AA:
SQ
Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 8, 9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLLVTSALAGORRGTQAESNLSSKFOFSSNKDONGVODPQHRITVSTNGSIHS 60.
DB 1 MSLEGLLLVTSALAGORGTQAESNLSSKFOFSSNKDONGVODPQHRITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLWRLVAEENWITQTDERGLDDEPDICKYPVEEESDGTIL 120
DB 61 PRPHYTPRNTVLWRLVAEENWITQTDERGLDDEPDICKYPVEEESDGTIL 120
QY 121 GRWGSCTVPCKQISKNQIRIRFVSDEYFPEEGFCIHYNIVMPQTEAVSPVLPPSA 180
DB 121 GRWGSCTVPCKQISKNQIRIRFVSDEYFPEEGFCIHYNIVMPQTEAVSPVLPPSA 180
QY 181 LPDLDLNNAITASTLEDLIRYLEPERWOLDLEDLYPTMQLGKAFVGRKSRVDLNL 240
DB 181 LPDLDLNNAITASTLEDLIRYLEPERWOLDLEDLYPTMQLGKAFVGRKSRVDLNL 240
QY 241 LEEVRLYSCTPRNFVSIREELKRTDTIFMPGCLYKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCTPRNFVSIREELKRTDTIFMPGCLYKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPTGVGLHKSLTDVALHNEECDCVCAGSTG 345
DB 301 VTKKYHEVLQLRPTGVGLHKSLTDVALHNEECDCVCAGSTG 345
RESULT 5
AA30023
ID AA30023 standard; Protein; 345 AA.
XX
XX AA30023:
AC
XX 11-OCT-1999 (first entry)
DT
XX
DE Human vascular endothelial growth factor related protein.
XX
XX Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
XX Homo sapiens.
OS
XX
XX WO9937671-A1.
PN
XX 29-JUL-1999.
PD
XX
XX 26-JAN-1999; 99WO-US01574.
PF
XX
XX 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0080809.
PR 24-JUN-1998; 98US-0090544.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Dou S, Na S, Song HY;
PI
XX

DR MPI: 1999-458680/38.
DR N-PSDB: AAX86352.
XX
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
XX
XX
SQ Sequence 345 AA:
Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
DB 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
QY 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFEVEEPPSDGTTIL 120
DB 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFEVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISGNQIRIFVSDYRPSRPGCIHNNIYMPQTEAVSSVLPSPA 180
DB 121 GRMGSGTVPGKQISGNQIRIFVSDYRPSRPGCIHNNIYMPQTEAVSSVLPSPA 180
QY 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTQQLGKAFVFRKSRVVDNL 240
DB 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTQQLGKAFVFRKSRVVDNL 240
QY 241 LITEVRLYSCTPRNFSVSIREEELKRTDTTFWPGCLLVKRCGACACCLHNCNCCVPSK 300
DB 241 LITEVRLYSCTPRNFSVSIREEELKRTDTTFWPGCLLVKRCGACACCLHNCNCCVPSK 300
QY 301 VTKKYEHLVQLRPKTVGRGLHKSITDVALEHHECCVCGSGTGG 345
DB 301 VTKKYEHLVQLRPKTVGRGLHKSITDVALEHHECCVCGSGTGG 345
RESULT 6
AAB48657
ID AAB48657 standard; Protein: 345 AA.
XX
XX AAB48657;
AC
XX
XX 09-MAR-2001 (first entry)
DT
XX
XX Human zvegfg3, SEQ ID NO:33.
DE
XX
XX Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnerrary; ischaemia;
KW immunomodulation; hepatic.
XX
XX Homo sapiens.
OS
XX
XX MO200066736-A1.
PN
XX
XX 09-NOV-2000.
PD
XX

PF 03-MAY-2000; 2000WO-US40047.
XX
XX 03-MAY-1999; 99US-0304216.
PR 10-NOV-1999; 99US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
XX (Zymo) ZYMOGENETICS INC.
PA
XX
XX Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
PI
XX
XX MPI: 2000-687541/67.
DR N-PSDB: AAC81582.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Claim 48; Page 125-126; 143pp; English.
XX
XX The invention relates to the human growth factor homologue zvegfg4
CC (AAB48653), and nucleic acids encoding it (AAC81555). zvegfg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. zvegfg4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. zvegfg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
CC fusions; expression constructs and host cells comprising human zvegfg4
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
CC which binds to human zvegfg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegfg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegfg4 gene of a patient. zvegfg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zvegfg3.
XX
XX
SQ Sequence 345 AA:
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
DB 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
QY 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFEVEEPPSDGTTIL 120
DB 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFEVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISGNQIRIFVSDYRPSRPGCIHNNIYMPQTEAVSSVLPSPA 180
DB 121 GRMGSGTVPGKQISGNQIRIFVSDYRPSRPGCIHNNIYMPQTEAVSSVLPSPA 180
QY 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTQQLGKAFVFRKSRVVDNL 240
DB 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTQQLGKAFVFRKSRVVDNL 240
QY 241 LITEVRLYSCTPRNFSVSIREEELKRTDTTFWPGCLLVKRCGACACCLHNCNCCVPSK 300
DB 241 LITEVRLYSCTPRNFSVSIREEELKRTDTTFWPGCLLVKRCGACACCLHNCNCCVPSK 300

QY 301 VTKKYEVLQLRPKTGVGRLHKSITDVALHHEECDCVCGSTGG 345
 |||||
 Db 301 VTKKYEVLQLRPKTGVGRLHKSITDVALHHEECDCVCGSTGG 345

RESULT 7
 AAB24250
 ID AAB24250 standard; Protein; 345 AA.
 XX
 AC AAB24250;

DT 08-FEB-2001 (first entry)
 XX
 DE Human platelet-derived growth factor related protein LP8.

XX
 KW Human; platelet derived growth factor related protein; LP8. VEGFh.
 KW vascular endothelial growth factor h; tissue regeneration; vulinerary;
 KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.

XX Homo sapiens.
 OS
 PN MO200059940-A2.

PD 12-OCT-2000.

PF 24-MAR-2000; 2000MO-US06427.

PR 06-APR-1999; 99US-0127913.

XX (ELIL) LILLY & CO ELI.

XX Hammond LJ, Na S;

DR MPI: 2000-664991/64.
 DR N-PSDB; AAC64426.

PT Enhancing tissue growth and promoting wound healing by administering
 platelet-derived growth factor related protein, LP8 or its analog and
 treating atherosclerosis by administering LP8 antagonist

XX Claim 4; Page 63-64; 64pp; English.

XX The present invention describes a method for enhancing tissue growth,
 CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated LP8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an LP8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth
 CC muscle growth. Antagonists of LP8 are useful for treating
 CC atherosclerosis. The present sequence represents human LP8, which is
 CC also called VEGFh.

XX Sequence 345 AA;

QY Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTALAGRRGTQAESNLSSKFQSSNKKQONGVODPQHRITTVSTNGSIHS 60
 |||||

Db 1 MSLEGLLVTALAGRRGTQAESNLSSKFQSSNKKQONGVODPQHRITTVSTNGSIHS 60

QY 61 PRPHPTPRNTVLMWLVAAVEENWIOITDERGLEDPEDDICKYFVEVEEESDGTIL 120
 |||||

Db 61 PRPHPTPRNTVLMWLVAAVEENWIOITDERGLEDPEDDICKYFVEVEEESDGTIL 120

QY 121 GRMGSGTGVGKQISKNQIRIRFVSDEFPSEPGFCIHYNIVMPOTFEAVSPVLPSSA 180
 |||||

Db 121 GRMGSGTGVGKQISKNQIRIRFVSDEFPSEPGFCIHYNIVMPOTFEAVSPVLPSSA 180

QY 181 LPDLNNATTAFTSTEDLIRYLEPERMOLDLEDLYRPTQLGKAFVFGKRSRVVDLNL 240
 |||||

Db 181 LPDLNNATTAFTSTEDLIRYLEPERMOLDLEDLYRPTQLGKAFVFGKRSRVVDLNL 240
 |||||

QY 241 LTEEVRLYSCTPRNFESVSTIEELKRTDTIFWPGCLLVKRCGACACCHNCNCCVPSK 300
 |||||

Db 241 LTEEVRLYSCTPRNFESVSTIEELKRTDTIFWPGCLLVKRCGACACCHNCNCCVPSK 300

QY 301 VTKKYEVLQLRPKTGVGRLHKSITDVALHHEECDCVCGSTGG 345
 |||||
 Db 301 VTKKYEVLQLRPKTGVGRLHKSITDVALHHEECDCVCGSTGG 345

RESULT 8
 AAB44322
 ID AAB44322 standard; Protein; 345 AA.
 XX
 AC AAB44322;

DT 08-FEB-2001 (first entry)

DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.

XX Homo sapiens.

PN MO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000MO-US04341.

PR 08-MAR-1999; 99MO-US05028.

PR 12-MAR-1999; 99US-0123857.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99MO-US28313.

PR 02-DEC-1999; 99MO-US28551.

PR 16-DEC-1999; 99MO-US30095.

PR 30-DEC-1999; 99MO-US31243.

PR 30-DEC-1999; 99MO-US31274.

PR 05-JAN-2000; 2000MO-US00219.

PR 06-JAN-2000; 2000MO-US00277.

PR 06-JAN-2000; 2000MO-US00376.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Petrarra N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillian KJ;

PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

DR MPI: 2000-611443/58.

DR N-PSDB; AAC78582.

PT Novel PRO polypeptides and polynucleotides used in detection methods,
 to target bioactive molecules to specific cells, and to modulate
 cellular activities

PS Claim 12; Fig 207; 636pp; English.

CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA:

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGILLTSLAGORGTQAESNLSKFOFSSNKEONGVODPOHERITTVSTNGSIHS 60
 DB 1 MSFLGILLTSLAGORGTQAESNLSKFOFSSNKEONGVODPOHERITTVSTNGSIHS 60
 QY 61 PREPHYPRNTVLMVRLVAEENVMWQLTFDERFGLEDEPEDICKDFVEVEPSDGTIL 120
 DB 61 PREPHYPRNTVLMVRLVAEENVMWQLTFDERFGLEDEPEDICKDFVEVEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLPSPA 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLPSPA 180
 QY 181 LPDLNLNMTAFSTLEDLIRYLEPERMQLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNLNMTAFSTLEDLIRYLEPERMQLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
 QY 241 LTFEEVRLVSCPTRNFSVSIREELKRTDTTFMPGCLLYKRCGNACCLINCEOCVPSK 300
 DB 241 LTFEEVRLVSCPTRNFSVSIREELKRTDTTFMPGCLLYKRCGNACCLINCEOCVPSK 300
 QY 301 VTKKYEVLQLRPKTGVRGLHSLTDVALEHHECDVCVCGSTGG 345
 DB 301 VTKKYEVLQLRPKTGVRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 9

ID AAB10633 standard; Protein: 345 AA.

XX AAB10633;

DT 19-JAN-2001 (first entry)

XX Human RACE generated VEGF-X protein.

XX VEGF-X: vascular endothelial growth factor; human; vulnerable; cytostatic;
 KW antiinflammatory; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99MO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;
 PI Dhanraj SM, Xu J;

DR WPI: 2000-442669/38.
 DR N-PSDB: AAB71951.

PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds .

XX Disclosure: Fig 6; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnerery, cytostatic, antiinflammatory, antipsoriatic, antidiabetic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antise molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation of tissues, tissue regeneration and organ
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the RACE generated human VEGF-X
 CC protein described in the method of the invention.

XX Sequence 345 AA:

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGILLTSLAGORGTQAESNLSKFOFSSNKEONGVODPOHERITTVSTNGSIHS 60
 DB 1 MSFLGILLTSLAGORGTQAESNLSKFOFSSNKEONGVODPOHERITTVSTNGSIHS 60
 QY 61 PREPHYPRNTVLMVRLVAEENVMWQLTFDERFGLEDEPEDICKDFVEVEPSDGTIL 120
 DB 61 PREPHYPRNTVLMVRLVAEENVMWQLTFDERFGLEDEPEDICKDFVEVEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLPSPA 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLPSPA 180
 QY 181 LPDLNLNMTAFSTLEDLIRYLEPERMQLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNLNMTAFSTLEDLIRYLEPERMQLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
 QY 241 LTFEEVRLVSCPTRNFSVSIREELKRTDTTFMPGCLLYKRCGNACCLINCEOCVPSK 300
 DB 241 LTFEEVRLVSCPTRNFSVSIREELKRTDTTFMPGCLLYKRCGNACCLINCEOCVPSK 300
 QY 301 VTKKYEVLQLRPKTGVRGLHSLTDVALEHHECDVCVCGSTGG 345
 DB 301 VTKKYEVLQLRPKTGVRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 10

ID AAB10635 standard; Protein: 345 AA.

XX AAB10635;

DT 19-JAN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

XX VEGF-X: vascular endothelial growth factor; human; vulnerable; cytostatic;
 KW antiinflammatory; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

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XX OS Homo sapiens.
XX PN WO200037641-A2.
XX PD 29-JUN-2000.
XX PF 21-DEC-1999; 99WO-US30503.
XX PR 22-DEC-1998; 98GB-0028377.
XX PR 18-MAR-1999; 99US-0124967.
XX PR 08-NOV-1999; 99US-0164131.
XX PA (JANC ) JANSSEN PHARM NV.
XX PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JHH, Goslowska A;
XX PI Dhanaraj SN, Xu J;
XX DR WPI: 2000-442669/38.
XX DR N-PSDB: AAA71955.
XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX PS Disclosure; Fig 9, 127pp; English.
XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX CC vulnerary, cyostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This sequence represents the human VEGF-X protein
XX CC isolated from clones 4 and 7 described in the method of the invention.
XX XX
XX SQ Sequence 345 AA:
XX
XX Query Match 99.6%; Score 1851; DB 21; Length 345;
XX Best Local Similarity 99.4%; Pred. No. 8.9e-179;
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
OY 61 PREPHYPRNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
DB 61 PREPHYPRNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
OY 121 GRMGCGTVPKQISKGNQIRIRFVSDPEFPPSGFCIHNIWMPQFTLEVSPVLPSSA 180
DB 121 GRMGCGTVPKQISKGNQIRIRFVSDPEFPPSGFCIHNIWMPQFTLEVSPVLPSSA 180
OY 181 LPLDLLNNAITAFSTLEDLIRYLEPERMQLDLEDLYRPTMQLGKAFVGRKSRVDLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERMQLDLEDLYRPTMQLGKAFVGRKSRVDLNL 240
OY 241 LEEVVALYCTPNSVSSTREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LEEVVALYCTPNSVSSTREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
OY 301 VAKKHYEVLQLRKRTGVGRGHKSLTDVALHHEECDCVGRSGNG 345
DB 301 VAKKHYEVLQLRKRTGVGRGHKSLTDVALHHEECDCVGRSGNG 345
OY 301 VAKKHYEVLQLRKRTGVGRGHKSLTDVALHHEECDCVGRSGNG 345
DB 301 VAKKHYEVLQLRKRTGVGRGHKSLTDVALHHEECDCVGRSGNG 345

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RESULT 11
AAB10644
ID AAB10644 standard; Protein; 345 AA.
XX AC AAB10644;
XX DT 19-JAN-2001 (first entry)
XX DE Human VEGF-X protein #4.
XX KW VEGF-X: vascular endothelial growth factor; human; vulnerary; cyostatic;
XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX KW venous sore; diabetic ulcer; burns; skin graft growth.
XX OS Homo sapiens.
XX PN WO200037641-A2.
XX PD 29-JUN-2000.
XX PF 21-DEC-1999; 99WO-US30503.
XX PR 22-DEC-1998; 98GB-0028377.
XX PR 18-MAR-1999; 99US-0124967.
XX PR 08-NOV-1999; 99US-0164131.
XX PA (JANC ) JANSSEN PHARM NV.
XX PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JHH, Goslowska A;
XX PI Dhanaraj SN, Xu J;
XX DR WPI: 2000-442669/38.
XX DR N-PSDB: AAA71955.
XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX PS Disclosure; Fig 30B; 127pp; English.
XX XX
XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX CC vulnerary, cyostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This sequence represents a human VEGF-X protein
XX CC described in the method of the invention.
XX XX
XX SQ Sequence 345 AA:
XX
XX Query Match 99.6%; Score 1851; DB 21; Length 345;
XX Best Local Similarity 99.4%; Pred. No. 8.9e-179;
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
OY 61 PREPHYPRNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
DB 61 PREPHYPRNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120

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|||||
Db 61 PREPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEDPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSPVLPSPA 180
    |||||||
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSPVLPSPA 180
QY 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVGRKSRVVDNL 240
    |||||||
Db 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTFEVRRLYSCTPRNFVSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
    |||||||
Db 241 LTFEVRRLYSCTPRNFVSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
QY 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCDVCCKSTGG 345
    |||||||
Db 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCDVCCKSTGG 345

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RESULT 12

AAB10650
ID AAB10650 standard; Protein; 345 AA.

AC AAB10650;

DT 19-JAN-2001 (first entry)

DE Human 990126vegx protein.

KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
 KW antihemmatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS MO200037641-A2.

PN 29-JUN-2000.

PD 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JH, Gosiowska A;

PI Dhanaraj SN, Xu J;

XX MPI; 2000-442669/38;

XX New vascular endothelial growth factor protein, useful for treating or

XX preventing diseases associated with inappropriate angiogenesis activity

XX such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX disclosure; Fig 11; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the human 990126vegx protein
 CC used to illustrate the method of the invention.

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;

Best Local Similarity 99.4%; Pred. No. 8.9e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGILLVTSALAGRGTOAESNLSSKRFQSSNKEONGVQDPQHERITVSTNGSIHS 60

Db 1 MSFLGILLVTSALAGRGTOAESNLSSKRFQSSNKEONGVQDPQHERITVSTNGSIHS 60

QY 61 PREPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEDPEDDICKYDFVEEPPSDGTTIL 120

Db 61 PREPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEDPEDDICKYDFVEEPPSDGTTIL 120

QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSPVLPSPA 180

Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSPVLPSPA 180

QY 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVGRKSRVVDNL 240

Db 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVGRKSRVVDNL 240

QY 241 LTFEVRRLYSCTPRNFVSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300

Db 241 LTFEVRRLYSCTPRNFVSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300

QY 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCDVCCKSTGG 345

Db 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCDVCCKSTGG 345

RESULT 13

AAB10651
ID AAB10651 standard; Protein; 345 AA.

AC AAB10651;

DT 19-JAN-2001 (first entry)

DE Human VEGF-X protein #3.

KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
 KW antihemmatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS MO200037641-A2.

PN 29-JUN-2000.

PD 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JH, Gosiowska A;

PI Dhanaraj SN, Xu J;

XX MPI; 2000-442669/38.

PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
 XX
 PS Claim 72: Fig 12; 127pp; English.
 XX
 CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (1a) and its encoding polynucleotide (1ia) which has
 CC vulnerrary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antiangiogenic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the human VEGF-X protein
 CC described in the method of the invention.
 CC
 XX
 SQ Sequence 345 AA:
 Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFGLLLVTSALAGORRQTOAESNLSSKFOFSSNKQNGVODPOHRIITVSTNGSIHS 60
 DB 1 MSFGLLLVTSALAGORRQTOAESNLSSKFOFSSNKQNGVODPOHRIITVSTNGSIHS 60
 QY 61 PRPHPTPRMTVLWRLVAVENWVIOITFDERGLDEPDIDCKYQVVEEESDSTIL 120
 DB 61 PRPHPTPRMTVLWRLVAVENWVIOITFDERGLDEPDIDCKYQVVEEESDSTIL 120
 QY 121 GRMGSGTVPKQISKNOIRIRFVSDSEYFSPGFCIHNIWVPOFTEAVSPSLPPSA 180
 DB 121 GRMGSGTVPKQISKNOIRIRFVSDSEYFSPGFCIHNIWVPOFTEAVSPSLPPSA 180
 QY 181 LPDLDLNNATTAFTSTEDLIRYLEPERWOLDLRYLPTWOLGKAFVFGKSRVVDLNL 240
 DB 181 LPDLDLNNATTAFTSTEDLIRYLEPERWOLDLRYLPTWOLGKAFVFGKSRVVDLNL 240
 QY 241 LTFEVRILYSCPRNFVSISIEBELKRTDTIFMPGCLLVKRGCGNACCLHNCNQCVPSPK 300
 DB 241 LTFEVRILYSCPRNFVSISIEBELKRTDTIFMPGCLLVKRGCGNACCLHNCNQCVPSPK 300
 QY 301 VTKKYEHLQLRPTGVGRLHKLSTDVLEHNEBCDCVCRGSTG 345
 DB 301 VTKKYEHLQLRPTGVGRLHKLSTDVLEHNEBCDCVCRGSTG 345
 RESULT 14
 AABI19578
 ID AABI19578 standard; Protein; 345 AA.
 XX
 AC AABI19578:
 DT 22-JAN-2001 (first entry)
 XX
 DE Human PRO200 (vascular endothelial growth factor E).
 XX
 KW PRO200: vascular epithelial growth factor E; VEGF-E; human;
 KW ocular disease; retinopathy; maculopathy; therapy;
 KW retinitis pigmentosa; macular degeneration; retinal detachment;
 KW retinal tear; macular hole; myopia; traumatic choroidretinopathy;
 KW acute retinal necrosis syndrome; contusion; edema;
 KW retinal vision occlusion; vascular disease; retinal vasculitis;
 KW thrombocytopenic purpura; uveitis; retinal occlusion.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..14
 FT Protein /label= Signal_Peptide
 FT 15..345
 FT Modified-site /label= Mature_Pro200
 FT 25..29
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 55..59
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 254..258
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 15..21
 FT Modified-site /note= "N-myristoylation"
 FT 117..123
 FT Modified-site /note= "N-myristoylation"
 FT 127..133
 FT Modified-site /note= "N-myristoylation"
 FT 281..287
 FT Modified-site /note= "N-myristoylation"
 FT 282..288
 FT Modified-site /note= "N-myristoylation"
 FT 319..325
 FT Modified-site /note= "Amidation"
 FT
 XX WO200053760-A2.
 XX
 XX 14-SEP-2000.
 XX
 XX 10-MAR-2000; 2000WO-US06319.
 XX
 XX 12-MAR-1999; 99US-0123957.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;
 PI Klein RD, Kljavin J, Kuo SS, La Fleur M, Wood WI;
 XX
 DR WPI: 2000-587437/55.
 DR N-PSDB; AAA88515.
 XX
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia,
 PT uveitis -
 XX
 PS Claim 2: Fig 2; 140pp; English.
 XX
 CC The present sequence is that of human PRO200 or vascular
 CC endothelial growth factor E (VEGF-E), as predicted from a cDNA
 CC clone (see AAA88515) that was isolated from a glioma cell line 661
 CC library using probes (see AAA88523-26) based on an expressed sequence
 CC tag (see AAA88522) that showed homology to VEGF. PRO200 has a
 CC predicted mol.wt. of 39,029 and a pI of about 6.06. A method for
 CC producing PRO polypeptides, including PRO200, using a host cell
 CC transformed with a vector comprising a PRO nucleic acid is claimed.
 CC The invention relates to the use of PRO polypeptides to delay,
 CC prevent or rescue retinal cells such as retinal neurons selected from
 CC photoreceptors, retinal ganglion cells, displaced retinal ganglion
 CC cells, amacrine cells, displaced amacrine cells, horizontal and
 CC bipolar neurons, and supportive cells (including Muller cells and
 CC pigment epithelial cells) from injury and degradation. The retinal
 CC cells are preferably photoreceptors and photoreceptor cell injury or
 CC death is caused by retinal injury, light or environmental trauma or
 CC by an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal
 CC tears, retinopathy, retinal degenerative diseases, macular holes,
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic
 CC choroidretinopathies or contusion such as Purtscher's retinopathy.
 CC edema, ischemic conditions such as central or branch retinal vision
 CC occlusion, collagen vascular diseases, thrombocytopenic purpura,
 CC uveitis, retinal vasculitis and occlusion associated with Fales
 CC disease and systemic lupus erythematosus (claimed).


```

XX  Sequence      345 AA:
SQ
Query Match      99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 MSLLGILLVTSALAGRCRQTAESNLSSKFQFSNNKEQGVODPOHERITITVSTNGSIHS 60
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DB  1 MSLLGILLVTSALAGRCRQTAESNLSSKFQFSNNKEQGVODPOHERITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  61 PPPPHYPRNTVLVWRLVAEENWVIQTLTDERFGLDEPDICKYDFVEVEEPPSDGTL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  61 PPPPHYPRNTVLVWRLVAEENWVIQTLTDERFGLDEPDICKYDFVEVEEPPSDGTL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  121 GWCMSGTVPGRQISKGNQIRIRFVSDEFEPEPFCIHYNIVMPQETAVSPSVLPSPA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  121 GWCMSGTVPGRQISKGNQIRIRFVSDEFEPEPFCIHYNIVMPQETAVSPSVLPSPA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  181 LPDLLNNATFASTLEDLIRYLEPERMQLDELDYRPTWQLGKAFVGRKSRVDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  181 LPDLLNNATFASTLEDLIRYLEPERMQLDELDYRPTWQLGKAFVGRKSRVDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  241 LTEEVRLISCTPRNFSVSIREELKRTDTITPQCCLVFKGNCACCLHNCBCCQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  241 LTEEVRLISCTPRNFSVSIREELKRTDTITPQCCLVFKGNCACCLHNCBCCQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  301 VVKKHEVQLRPKTVGRGLHKSITDVNLEHHHECCDVCGRSGTG 345
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DB  301 VVKKHEVQLRPKTVGRGLHKSITDVNLEHHHECCDVCGRSGTG 345
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RESULT 15
AAB33414
ID  AAB33414 standard: Protein: 345 AA.
XX
AC  AAB33414;
XX
DT  29-JAN-2001 (first entry)
XX
DE  Human PRO200 protein UNO174 SEQ ID NO:2.
XX
KW  Human; immune related disease; diagnosis; antinflammatory; cardiant;
    dermatological; ankylosing; antineuritic; immunosuppressive;
    haemostatic; antithyroid; antidiabetic; nocrotic; neuroprotective;
    antianemic; hepatotropic; virucide; antiparasitic; anti-allergic;
    antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
    osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
    idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
    systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
    autoimmune thrombocytopenia; immune-mediated renal disease;
    demyelinating disease; hepatobiliary disease; Whipple's disease;
    inflammatory bowel disease; gluten-sensitive enteropathy;
    autoimmune disease; immune-mediated skin disease; allergic disease;
    immunological disease; transplantation associated disease;
    graft rejection; graft-versus-host-disease.
XX
OS  Homo sapiens.
XX
PN  WO200053756-A2.
XX
PD  14-SEP-2000.
XX
PF  02-MAR-2000; 2000WO-US05841.
XX
PR  08-MAR-1999; 99WO-US05028.
    10-MAR-1999; 99US-0123618.
    12-MAR-1999; 99US-0123957.
    12-MAR-1999; 99US-0125775.
    12-APR-1999; 99US-0128849.
    20-APR-1999; 99WO-US08615.
    28-APR-1999; 99US-0131445.
    04-MAY-1999; 99US-0133371.

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PR  14-MAY-1999; 99US-0134287.
PR  02-JUN-1999; 99WO-US12252.
PR  23-JUN-1999; 99US-0141037.
PR  20-JUL-1999; 99US-0144758.
PR  26-JUL-1999; 99US-0145698.
PR  28-JUL-1999; 99US-0146222.
PR  01-SEP-1999; 99WO-US20111.
PR  08-SEP-1999; 99WO-US20594.
PR  13-SEP-1999; 99WO-US20944.
PR  15-SEP-1999; 99WO-US21090.
PR  15-SEP-1999; 99WO-US21547.
PR  05-OCT-1999; 99WO-US23089.
PR  29-OCT-1999; 99US-0162506.
PR  29-NOV-1999; 99WO-US28214.
PR  30-NOV-1999; 99WO-US28313.
PR  30-NOV-1999; 99WO-US28309.
PR  01-DEC-1999; 99WO-US28301.
PR  01-DEC-1999; 99WO-US28634.
PR  02-DEC-1999; 99WO-US28551.
PR  02-DEC-1999; 99WO-US28564.
PR  16-DEC-1999; 99WO-US30095.
PR  20-DEC-1999; 99WO-US30999.
PR  30-DEC-1999; 99WO-US31274.
PR  05-JAN-2000; 2000WO-US00219.
PR  06-JAN-2000; 2000WO-US00277.
PR  06-JAN-2000; 2000WO-US00376.
PR  11-FEB-2000; 2000WO-US03565.
PR  18-FEB-2000; 2000WO-US04341.
PR  18-FEB-2000; 2000WO-US04342.
PR  22-FEB-2000; 2000WO-US04414.
XX
XX  (GENTH ) GENENTECH INC.
XX
PA  Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI  Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI  Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
XX  WPI: 2000-572271/53.
XX  N-PSDB: AAC58579.
XX
DR  Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX  immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX  arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
XX  Claim 33; Fig 2; 309pp; English.
XX
XX  The present invention describes sixty four human PRO proteins which can
XX  be used in the treatment of immune related diseases. The human PRO
XX  proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX  treating and diagnosing immune related disorders. The disorders are
XX  selected from systemic lupus erythematosus, rheumatoid arthritis,
XX  osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
XX  systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX  syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX  anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX  immune-mediated renal disease, demyelinating diseases of the central
XX  and peripheral nervous systems, hepatobiliary diseases, inflammatory
XX  bowel disease, gluten-sensitive enteropathy and Whipple's disease,
XX  autoimmune or immune-mediated skin diseases, allergic diseases,
XX  immunological diseases of the lung, and transplantation associated
XX  diseases including graft rejection and graft-versus-host-disease.
XX  AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
XX  in the isolation of human PRO sequences. AAC58579 to AAC58642 and
XX  AAB33414 to AAB33477 represent human PRO polynucleotide and protein
XX  sequences given in the exemplification of the present invention.
XX
SQ  Sequence      345 AA:

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Query Match      99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Oy	61	PRFPHTYPRNTVLWRLVAEENWVIOLTJFERGRLGEDPEDDICKYDFVEEPPSDGTLI	120
Dd	61	PRFPHTYPRNTVLWRLVAEENWVIOLTJFERGRLGEDPEDDICKYDFVEEPPSDGTLI	120
Oy	121	GRMCGSGTVPKQKJOSKGNQIRIRFVSDSEYFPSEBFGCIHYNIVMPQTEAVSPSVLPPSA	180
Dd	121	GRMCGSGTVPKQKJOSKGNQIRIRFVSDSEYFPSEBFGCIHYNIVMPQTEAVSPSVLPPSA	180
Oy	181	LPRLDLNNAITAESEDLIRYLEPERWQDLEDLRYPTQMLLGKAPVGRKSRVVDNLV	240
Dd	181	LPRLDLNNAITAESEDLIRYLEPERWQDLEDLRYPTQMLLGKAPVGRKSRVVDNLV	240
Oy	241	LTEEVRALYSCPRNPNVSIREELKRTPTIPWPGLLYKRCGGNACACILHNCNCCQVPSK	300
Dd	241	LTEEVRALYSCPRNPNVSIREELKRTPTIPWPGLLYKRCGGNACACILHNCNCCQVPSK	300
Oy	301	VTYKKNHEVLOLRPTGVAGLKSJLTVDALHNHEBCDCVCGSGTGG	345
Dd	301	VTYKKNHEVLOLRPTGVAGLKSJLTVDALHNHEBCDCVCGSGTGG	345

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Job time : 34.5 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:08:16 ; Search time 26.5 seconds
(without alignments)
1043.199 Million cell updates/sec

Title: US-09-818-943-1

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications-AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1858	100.0	345	9	US-10-086-623-32
3	1858	100.0	345	9	US-10-260-539-32
4	1858	100.0	345	10	US-09-818-943-1
5	1851	99.6	345	9	US-09-978-295A-488
6	1851	99.6	345	9	US-09-978-697-488
7	1851	99.6	345	9	US-09-978-192A-488
8	1851	99.6	345	9	US-10-139-583-2
9	1851	99.6	345	9	US-09-999-832A-488
10	1851	99.6	345	9	US-09-878-189-488
11	1851	99.6	345	9	US-10-028-072-286
12	1851	99.6	345	9	US-10-121-049-286
13	1851	99.6	345	9	US-10-123-904-286
14	1851	99.6	345	9	US-10-140-470-286
15	1851	99.6	345	9	US-09-796-753-6
16	1851	99.6	345	9	US-10-175-746-286
17	1851	99.6	345	9	US-10-176-918-286
18	1851	99.6	345	9	US-10-176-921-286
19	1851	99.6	345	9	US-10-103-197-4

20	1851	99.6	345	9	US-10-137-865-286	Sequence 286, App
21	1851	99.6	345	9	US-10-140-474-286	Sequence 286, App
22	1851	99.6	345	9	US-10-142-431-286	Sequence 286, App
23	1851	99.6	345	9	US-10-143-114-286	Sequence 286, App
24	1851	99.6	345	9	US-10-140-002-286	Sequence 286, App
25	1851	99.6	345	9	US-09-978-608A-488	Sequence 488, App
26	1851	99.6	345	9	US-10-142-419-286	Sequence 286, App
27	1851	99.6	345	9	US-09-978-191A-488	Sequence 488, App
28	1851	99.6	345	9	US-09-978-403A-488	Sequence 488, App
29	1851	99.6	345	9	US-09-878-564A-488	Sequence 488, App
30	1851	99.6	345	9	US-09-978-585A-488	Sequence 488, App
31	1851	99.6	345	9	US-10-017-081A-488	Sequence 488, App
32	1851	99.6	345	9	US-10-123-262-286	Sequence 286, App
33	1851	99.6	345	9	US-10-142-423-286	Sequence 286, App
34	1851	99.6	345	9	US-09-978-824-488	Sequence 488, App
35	1851	99.6	345	9	US-09-981-915A-488	Sequence 488, App
36	1851	99.6	345	9	US-09-999-833A-488	Sequence 488, App
37	1851	99.6	345	9	US-10-121-050-286	Sequence 286, App
38	1851	99.6	345	9	US-10-141-755-286	Sequence 286, App
39	1851	99.6	345	9	US-10-167-749-488	Sequence 488, App
40	1851	99.6	345	9	US-09-918-585A-488	Sequence 488, App
41	1851	99.6	345	9	US-10-143-032-286	Sequence 286, App
42	1851	99.6	345	9	US-09-978-423A-488	Sequence 488, App
43	1851	99.6	345	9	US-10-013-921A-488	Sequence 488, App
44	1851	99.6	345	9	US-10-123-108-286	Sequence 286, App
45	1851	99.6	345	9	US-10-123-236-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-852-209A-3

Sequence 3, Application US/09852209A

Patent No. US20020164687A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, ULF

APPLICANT: AASE, Karin

APPLICANT: LEF, Xuri

APPLICANT: FONTEN, Annica

APPLICANT: DUFELO, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Anne

APPLICANT: HELDIN, Carl-Henrik

APPLICANT: BETHSHOLTZ, Christer

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

FILE REFERENCE: THEREFOR, AND USES THEREOF

CURRENT APPLICATION NUMBER: 09-410349-Eriksson et al-1064-44740

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 09/410,349

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/110,749

PRIOR FILING DATE: 1998-12-03

PRIOR APPLICATION NUMBER: 60/113,002

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: 60/135,426

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: 60/144,022

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-09-852-209A-3

Query Match 100.0% Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLGILLVTSALAGORNGTGAESNLSSKRFQFSSNKEQNGVQDPQHEIRITVSTNSINS 60

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Db 1 MSFGLLTVSALAGORGTQAESNLSSKFOFSSNKQNGVOPQHRITTVSNGSIHS 60
QY 61 PREPHYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
Db 61 PREPHYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
QY 121 GRMGSGTVGKQISKNOQIRIRFVSDEYFPESEFGCIHNIYMPQTEAVSPVLPPSA 180
Db 121 GRMGSGTVGKQISKNOQIRIRFVSDEYFPESEFGCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVDNL 240
Db 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVDNL 240
QY 241 LEEVRLYSTCPNRFVSISIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
Db 241 LEEVRLYSTCPNRFVSISIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
QY 301 VTKKHEVLQLRPKTGVGRLHKSITDVALHHEBCDCVCRGSGTG 345
Db 301 VTKKHEVLQLRPKTGVGRLHKSITDVALHHEBCDCVCRGSGTG 345
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RESULT 2
US-10-086-623-32
; Sequence 32, Application US/10086623
; Patent No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: MASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32
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Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MSFGLLTVSALAGORGTQAESNLSSKFOFSSNKQNGVOPQHRITTVSNGSIHS 60
Db 1 MSFGLLTVSALAGORGTQAESNLSSKFOFSSNKQNGVOPQHRITTVSNGSIHS 60
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QY 61 PREPHYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
Db 61 PREPHYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120
QY 121 GRMGSGTVGKQISKNOQIRIRFVSDEYFPESEFGCIHNIYMPQTEAVSPVLPPSA 180
Db 121 GRMGSGTVGKQISKNOQIRIRFVSDEYFPESEFGCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVDNL 240
Db 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVDNL 240
QY 241 LEEVRLYSTCPNRFVSISIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
Db 241 LEEVRLYSTCPNRFVSISIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
QY 301 VTKKHEVLQLRPKTGVGRLHKSITDVALHHEBCDCVCRGSGTG 345
Db 301 VTKKHEVLQLRPKTGVGRLHKSITDVALHHEBCDCVCRGSGTG 345
```

```
RESULT 3
US-10-260-539-32
; Sequence 32, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: MASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32
```

```
Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MSFGLLTVSALAGORGTQAESNLSSKFOFSSNKQNGVOPQHRITTVSNGSIHS 60
Db 1 MSFGLLTVSALAGORGTQAESNLSSKFOFSSNKQNGVOPQHRITTVSNGSIHS 60
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Qy	61	PRPHYTPRNTVLVWRYVAEENWIDLTDERGLEDPEDDICXKDFVEEPPSGTIL	120
Db	61	PRPHYTPRNTVLVWRYVAEENWIDLTDERGLEDPEDDICXKDFVEEPPSGTIL	120
Qy	121	GRMGSGTVPFGKOISKNOQIRIRFVSDEYFSEBFGCIHYNVMPQTEAVSESVLPSSA	180
Db	121	GRMGSGTVPFGKOISKNOQIRIRFVSDEYFSEBFGCIHYNVMPQTEAVSESVLPSSA	180
Qy	181	LPDLNLNNTAATFSTEDLIRYLEPEEMOLDLBYRPTQMLGKFAVFEGRKSRVVDNL	240
Db	181	LPDLNLNNTAATFSTEDLIRYLEPEEMOLDLBYRPTQMLGKFAVFEGRKSRVVDNL	240
Qy	241	LTEEVRLYSCTPRNFVSYSIREELKRTDTIIPWGLLYKRCGACACILHNCNCECVPSK	300
Db	241	LTEEVRLYSCTPRNFVSYSIREELKRTDTIIPWGLLYKRCGACACILHNCNCECVPSK	300
Qy	301	VTKKYYHEVLDRPKTVGRGLHKLSTVDALHHNECCVCGVSGTGG	345
Db	301	VTKKYYHEVLDRPKTVGRGLHKLSTVDALHHNECCVCGVSGTGG	345

```

RESULT 4
US-09-818-943-1
: Sequence 1, Application US/09818943
: Patent No. US20020049987A1
: GENERAL INFORMATION:
: APPLICANT: ERIKSSON, Ulf
: APPLICANT: LI, Xuri
: APPLICANT: PONTEN, Annika
: APPLICANT: AASE, Karin
: APPLICANT: LI, Hong
: TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
: TITLE OF INVENTION: (PDF-C) AND USES THEREOF
: FILE REFERENCE: 1064/48487
: CURRENT APPLICATION NUMBER: US/09/818,943
: CURRENT FILING DATE: 2001-03-28
: PRIOR APPLICATION NUMBER: US 60/192,507
: PRIOR FILING DATE: 2000-03-28
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 1
: LENGTH: 345
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-09-818-943-1

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Query Match	100.0%;	Score 1858;	DB 10;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 2, 6e-161;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSLGLLLVSALAGORRGTOAESNLSSKFPSSKKEONGVODPOHERITTVSTNGSIHS	60	
Db	1	MSLGLLLVSALAGORRGTOAESNLSSKFPSSKKEONGVODPOHERITTVSTNGSIHS	60	
QY	61	PRPHTPRNTVLVWRLVAVEENWIOLTPEBREGLEPEDDICKYDVEVEEESDGTLL	120	
Db	61	PRPHTPRNTVLVWRLVAVEENWIOLTPEBREGLEPEDDICKYDVEVEEESDGTLL	120	
QY	121	GRMGSGTVPKQKISKGNQIRIRIREVSDSEYFPESEFGCIHYNIYVMQFTAEVASSVLPPSA	180	
Db	121	GRMGSGTVPKQKISKGNQIRIRIREFSDSEYFPESEFGCIHYNIYVMQFTAEVASSVLPPSA	180	
QY	181	LPDLNLNNAITAFSTLEDELIRYLEPERKQOLDLEDLRPTWOLLGAAPYFGKRSRYVDLNL	240	
Db	181	LPDLNLNNAITAFSTLEDELIRYLEPERKQOLDLEDLRPTWOLLGAAPYFGKRSRYVDLNL	240	
QY	241	LTEEVRLTSCPTPRNFSVSIREEIKRTDPIIFMPGCLTVRCGNCACCLHNCNECCQCPFSK	300	
Db	241	LTEEVRLTSCPTPRNFSVSIREEIKRTDPIIFMPGCLTVRCGNCACCLHNCNECCQCPFSK	300	
QY	301	VTKKYHYEVLQRPYTGVRGLHKLSTDLVALHEHNECCDVCYCRSGTGG	345	

Db 301 VTKKXHEVLQRPKTVGVLHKSJLTDVALHEHNECSDCVRSGTSG 345

RESULT 5
US-09-978-295A-488
Sequence 488, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavina, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/079923
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080334
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081952
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
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;; PRIOR FILING DATE: 1998-04-21
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;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR APPLICATION NUMBER: 60/083495
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;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR APPLICATION NUMBER: 60/085700
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLFGLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVQDPQHRITTVSTNGSIHS 60
DB 1 MSLLFGLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVQDPQHRITTVSTNGSIHS 60
QY 61 PRPHPTVPRNTVLVWIRVAAEENVMWIOLEFDERFGLEDPEDDICKYDFVEEPPSGTTL 120
DB 61 PRPHPTVPRNTVLVWIRVAAEENVMWIOLEFDERFGLEDPEDDICKYDFVEEPPSGTTL 120
QY 121 GRWGSCTVPGKOTSGNQIIRFVSDVEYFPPSEPGCIHYNIMVQFTTEAVSPSVLPESA 180

Db 121 GRWGSOTVGGKQISKNOQIRFVSDEYFPPSEPGFICIHNYIMPOFTEAVSPSVLEPSPA 180
Qy 181 LPIDLNNATATSTLEDDLRLYLEPERWOLDLDIARPTMOLLGKAFVGRKSRVVDLNL 240
Db 181 LPIDLNNATATSTLEDDLRLYLEPERWOLDLDIARPTMOLLGKAFVGRKSRVVDLNL 240
Qy 241 LTEEVRLYSTCPNRFVSYSINEELKRDITIPWPGCLLYKRCGNCACCLAHNCNCCQVPSK 300
Db 241 LTEEVRLYSTCPNRFVSYSINEELKRDITIPWPGCLLYKRCGNCACCLAHNCNCCQVPSK 300
Qy 301 VTKKYHEVLDLRKPTGVRGLHKSLLTDVLALEHHEBCDCVCRGTGG 345
Db 301 VTKKYHEVLDLRKPTGVRGLHKSLLTDVLALEHHEBCDCVCRGTGG 345

RESULT 6
US-09-978-697-488
Sequence 488, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFGLLVTSALAGRGQDAESNLSSKFOFSSNKQNGVQDPQHRITTVTSNGSIHS 60
Db 1 MSFGLLVTSALAGRGQDAESNLSSKFOFSSNKQNGVQDPQHRITTVTSNGSIHS 60
QY 61 PRPHYTPRNTVLVWRLVAEENWVQLTFDERGLEDPEDDICKYQFVVEEPPSDGTL 120
Db 61 PRPHYTPRNTVLVWRLVAEENWVQLTFDERGLEDPEDDICKYQFVVEEPPSDGTL 120
QY 121 GRMGSGTVPGKQISKNOIRIRFVSDPEPSEPCFIHNYIWPQTEAVSPSLPPSA 180
Db 121 GRMGSGTVPGKQISKNOIRIRFVSDPEPSEPCFIHNYIWPQTEAVSPSLPPSA 180
QY 181 LPDDLNNATTAFTSLDLIRYLEPERWQDLEDLYPTWQLGKAVFGKRSKRVYDNL 240
Db 181 LPDDLNNATTAFTSLDLIRYLEPERWQDLEDLYPTWQLGKAVFGKRSKRVYDNL 240
QY 241 LTFEVRLYSCTPRNFVSIRBELKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTFEVRLYSCTPRNFVSIRBELKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTGVGRLKSLTDVALEHNEHCDCVCRGSTG 345
Db 301 VTKKYHEVLQLRPKTGVGRLKSLTDVALEHNEHCDCVCRGSTG 345

RESULT 7
US-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavan, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978, 192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHPTPRNTVLWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
DB 61 PRPHPTPRNTVLWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVPGKQISKQNRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKQISKQNRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDILLNNAITAESTDLDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
DB 181 LPDILLNNAITAESTDLDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
QY 241 LTFEVRLYSCTPRNFVSITREELKRTDTIFWPGCLLYKRCGNCACCLHNCNEQCVPSK 300
DB 241 LTFEVRLYSCTPRNFVSITREELKRTDTIFWPGCLLYKRCGNCACCLHNCNEQCVPSK 300
QY 301 VTKKYHEVLQLRPTGVRLHKSITDVALEHHECCDCVCGSTG 345
DB 301 VTKKYHEVLQLRPTGVRLHKSITDVALEHHECCDCVCGSTG 345

RESULT 8
US-10-139-583-2
; Sequence 2, Application US/10139583
; Patent No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-2

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVDPQHERIITVSTNGSIHS 60

DB 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPHPTPRNTVLWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
DB 61 PRPHPTPRNTVLWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVPGKQISKQNRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKQISKQNRIRFVSDYFPPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDILLNNAITAESTDLDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
DB 181 LPDILLNNAITAESTDLDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
QY 241 LTFEVRLYSCTPRNFVSITREELKRTDTIFWPGCLLYKRCGNCACCLHNCNEQCVPSK 300
DB 241 LTFEVRLYSCTPRNFVSITREELKRTDTIFWPGCLLYKRCGNCACCLHNCNEQCVPSK 300
QY 301 VTKKYHEVLQLRPTGVRLHKSITDVALEHHECCDCVCGSTG 345
DB 301 VTKKYHEVLQLRPTGVRLHKSITDVALEHHECCDCVCGSTG 345

RESULT 9
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGQRTOAESNLSSKRFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLEGLLVTSALAGRGQRTOAESNLSSKRFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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DB 61 PREPHTYPRNTVWRLVAVAEENWVQLTDERGLEDDEDDICKYDFVEEESDGIIL 120
QY 121 GRMGSGTVGKQJISKNQIRIRFVSDPEPFCIHYNITVMPQFTFAVSPVLPPSA 180
DB 121 GRMGSGTVGKQJISKNQIRIRFVSDPEPFCIHYNITVMPQFTFAVSPVLPPSA 180
QY 181 LPDLDLNNATFASTEDLDLRYLEPERWQDLEDLYRPTWQLGKAEVFGKRSVVDLNL 240
DB 181 LPDLDLNNATFASTEDLDLRYLEPERWQDLEDLYRPTWQLGKAEVFGKRSVVDLNL 240
QY 241 LTFEVRILYSCPRNFVSIREELKRTDTIFWPGLLYKRCGGNACCLHNCNEQCVPSK 300
DB 241 LTFEVRILYSCPRNFVSIREELKRTDTIFWPGLLYKRCGGNACCLHNCNEQCVPSK 300
QY 301 VTKKYHEVLQLRPKTGVGLHKSLLDVALEHHECDVCVCRSGTG 345
DB 301 VTKKYHEVLQLRPKTGVGLHKSLLDVALEHHECDVCVCRSGTG 345

RESULT 10
US-09-978-189-488
; Sequence 488, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: F2630PIC7
; CURRENT APPLICATION NUMBER: US/09/978,189

;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
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;; PRIOR FILING DATE: 1998-04-08

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PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSLEGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVVEENWVQLTFDERFGLDEPEDICXYDFVEVEPSDGTLL 120
DB 61 PREPHTYPRNTVLVWRLVVEENWVQLTFDERFGLDEPEDICXYDFVEVEPSDGTLL 120
QY 121 GWCSSGTVPGKQISKGNQIRIRFVSDEFPSPEPGCHINYNMPOFTFVAVSPVLPSPA 180
DB 121 GWCSSGTVPGKQISKGNQIRIRFVSDEFPSPEPGCHINYNMPOFTFVAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDIRYLEPERWOLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDIRYLEPERWOLDLEDLYRPTWOLLGKAFVGRKSRVVDLNL 240
QY 241 LEEVRLVYSCPTPRNFVSISREELKRTDITFWPGCLLVKRCGNACCLHNCNECCVPSK 300
DB 241 LEEVRLVYSCPTPRNFVSISREELKRTDITFWPGCLLVKRCGNACCLHNCNECCVPSK 300
QY 301 VTKKYHEVLQLRPKTGVRLKSLTDVALEHHEEDCCVCRSGTGG 345
DB 301 VTKKYHEVLQLRPKTGVRLKSLTDVALEHHEEDCCVCRSGTGG 345

RESULT 11
US-10-028-072-286
Sequence 286, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08614
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026

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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
```

Query Match 99.6%; Score 1851; DB 9; Length 345;

Best Local Similarity 99.4%; Pred. No. 1.1e-160; Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
DB 1 MSFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
QY 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
QY 121 GRMGSGTYPGKQISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
DB 121 GRMGSGTYPGKQISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDILRYLEPERWQDLLEDLYRPTWQLLGAFAVGRKSRVVDNL 240
DB 181 LPDLLNNAITAFSTLEDILRYLEPERWQDLLEDLYRPTWQLLGAFAVGRKSRVVDNL 240
QY 241 LEEVRLYSTPRNFSVSIREELKRTDTJFWPGCLLYKRCGNCACCLHNCCOCVPSK 300
DB 241 LEEVRLYSTPRNFSVSIREELKRTDTJFWPGCLLYKRCGNCACCLHNCCOCVPSK 300
QY 301 VTKKYEVLQLRPKTVGRGLHKSJLTDVALEHHECCDCVCRGSTGG 345
DB 301 VTKKYEVLQLRPKTVGRGLHKSJLTDVALEHHECCDCVCRGSTGG 345
```

RESULT 12

```

US-10-121-049-286
; Sequence 286, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-286
```

Query Match 99.6%; Score 1851; DB 9; Length 345;

Best Local Similarity 99.4%; Pred. No. 1.1e-160; Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
DB 1 MSFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
QY 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120
QY 121 GRMGSGTYPGKQISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
DB 121 GRMGSGTYPGKQISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDILRYLEPERWQDLLEDLYRPTWQLLGAFAVGRKSRVVDNL 240
DB 181 LPDLLNNAITAFSTLEDILRYLEPERWQDLLEDLYRPTWQLLGAFAVGRKSRVVDNL 240
QY 241 LEEVRLYSTPRNFSVSIREELKRTDTJFWPGCLLYKRCGNCACCLHNCCOCVPSK 300
DB 241 LEEVRLYSTPRNFSVSIREELKRTDTJFWPGCLLYKRCGNCACCLHNCCOCVPSK 300
QY 301 VTKKYEVLQLRPKTVGRGLHKSJLTDVALEHHECCDCVCRGSTGG 345
DB 301 VTKKYEVLQLRPKTVGRGLHKSJLTDVALEHHECCDCVCRGSTGG 345
```

RESULT 13

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US-10-123-904-286
; Sequence 286, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
```

```

; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-904-286

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGORRGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSLEGLLVTSALAGORGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREPHTYPRNTVLWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
QY 181 LPDLDLNNATTAESTLEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVGRKSRVVDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LPDLDLNNATTAESTLEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTEEVRILYSCTPRNFVSISIEELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LTEEVRILYSCTPRNFVSISIEELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQVPSK 300
QY 301 VTKKYEVLQLRPTGVRLHKSITDVALHHEECDCVCGSGTGG 345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKYEVLQLRPTGVRLHKSITDVALHHEECDCVCGSGTGG 345

RESULT 14
US-10-140-470-286
; Sequence 286, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-470-286

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGORRGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSLEGLLVTSALAGORGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREPHTYPRNTVLWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEPGFCIHNIYVPOFTEAVSPSVLPSSA 180
QY 181 LPDLDLNNATTAESTLEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVGRKSRVVDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LPDLDLNNATTAESTLEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVGRKSRVVDNL 240
QY 241 LTEEVRILYSCTPRNFVSISIEELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LTEEVRILYSCTPRNFVSISIEELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQVPSK 300
QY 301 VTKKYEVLQLRPTGVRLHKSITDVALHHEECDCVCGSGTGG 345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKYEVLQLRPTGVRLHKSITDVALHHEECDCVCGSGTGG 345

RESULT 15
US-09-796-753-6
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION REMOVED: 09/471,179
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;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: 09/474,071
;; PRIOR FILING DATE: 1999-12-29
;; PRIOR APPLICATION NUMBER: 09/474,072
;; PRIOR FILING DATE: 1999-12-29
;; PRIOR APPLICATION NUMBER: 09/514,010
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 09/516,745
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/572,002
;; PRIOR FILING DATE: 2000-05-14
;; PRIOR APPLICATION NUMBER: 09/597,993
;; PRIOR FILING DATE: 2000-06-19
;; PRIOR APPLICATION NUMBER: 09/599,596
;; PRIOR FILING DATE: 2000-06-22
;; PRIOR APPLICATION NUMBER: 09/630,334
;; PRIOR FILING DATE: 2000-07-31
;; PRIOR APPLICATION NUMBER: 09/606,565
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: 09/606,317
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: 09/665,666
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: 09/677,751
;; PRIOR FILING DATE: 2000-09-30
;; NUMBER OF SEQ ID NOS: 162
;; SEQ ID NO 6
;; LENGTH: 345
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-796-753-6

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSIFGLLTVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVSTNGSIHS 60
Db 1 MSIFGLLTVTSALAGRGTOAESNLSSKQFSSNKQNGVODPOHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
Db 61 PREPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
QY 121 GRWCGGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180
Db 121 GRWCGGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180
QY 181 LPLDLNNAITAFSTLEDLIRYLEPFRWOLDLDRPTWOLGKAFFGKRSRVVDNL 240
Db 181 LPLDLNNAITAFSTLEDLIRYLEPFRWOLDLDRPTWOLGKAFFGKRSRVVDNL 240
QY 241 LTEEVRLYCTPRNFSVSIRBELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRLYCTPRNFSVSIRBELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVQLRPKTGVRGLHSLTDVALEHHHECCDVCGRSTGG 345
Db 301 VTKKYHEVQLRPKTGVRGLHSLTDVALEHHHECCDVCGRSTGG 345

Search completed: April 29, 2003, 09:16:55
Job time : 27.5 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:03:41 ; Search time 55 Seconds
(without alignments)
1292.477 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSIFGLLVTSALAGQRGT.....DVLEHHEBCDCVCRGTSG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organellar:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1858	100.0	345	Q9NRAL	Q9NRAL homo sapien
2	1851	99.6	345	Q9UL22	Q9UL22 homo sapien
3	1664	89.6	345	Q9QY71	Q9QY71 mus musculus
4	1646	88.6	345	Q9EQX6	Q9EQX6 rattus norv
5	1635	88.0	345	Q9JH8	Q9JH8 mus musculus
6	1614	86.9	345	Q91946	Q91946 gallus galli
7	741.5	39.9	370	Q9GZP0	Q9GZP0 homo sapien
8	740.5	39.9	364	Q9BWS	Q9BWS homo sapien
9	737.5	39.7	370	Q92517	Q92517 mus musculus
10	736	39.6	370	Q9EQ71	Q9EQ71 rattus norv
11	645	34.7	290	Q9D1L8	Q9D1L8 mus musculus
12	190.5	10.3	923	Q9OFP6	Q9OFP6 brachydantio
13	183	9.8	3623	Q9O494	Q9O494 homo sapien
14	182	9.8	691	Q97658	Q97658 gallus galli
15	180	9.7	34	Q99JH4	Q99JH4 mus musculus
16	176	9.5	977	Q91925	Q91925 xenopus lae

17	176	9.5	3623	11	Q70244	Q70244 rattus norv
18	172	9.3	1012	11	Q9WVM6	Q9WVM6 mus musculus
19	171	9.2	735	13	Q57381	Q57381 xenopus lae
20	171	9.2	926	4	Q9UQ00	Q9UQ00 homo sapien
21	171	9.2	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
22	169	9.1	241	11	Q92135	Q92135 rattus norv
23	165.5	8.9	555	4	Q8Q2Y7	Q8Q2Y7 mus musculus
24	164.5	8.9	555	4	Q9H2E2	Q9H2E2 homo sapien
25	164.5	8.9	901	4	Q9H2E4	Q9H2E4 homo sapien
26	164.5	8.9	901	4	Q9H2D5	Q9H2D5 homo sapien
27	164.5	8.9	906	4	Q9H2E3	Q9H2E3 homo sapien
28	164.5	8.9	906	4	Q9H2D4	Q9H2D4 homo sapien
29	163.5	8.8	921	11	Q9QX38	Q9QX38 rattus norv
30	163.5	8.8	3620	6	Q9RU53	Q9RU53 canis famill
31	158.5	8.5	609	4	Q96190	Q96190 homo sapien
32	158.5	8.5	644	4	Q961H5	Q961H5 homo sapien
33	158.5	8.5	704	4	Q9H2E1	Q9H2E1 homo sapien
34	157.5	8.5	919	13	Q8UVRO	Q8UVRO gallus galli
35	157.5	8.5	936	13	Q8UVQ9	Q8UVQ9 gallus galli
36	157	8.4	1008	13	Q9DER7	Q9DER7 gallus galli
37	153	8.2	415	4	Q9UKZ9	Q9UKZ9 homo sapien
38	153	8.2	1019	13	Q57382	Q57382 xenopus lae
39	151.5	8.2	326	11	Q91ZE4	Q91ZE4 rattus norv
40	151	8.1	276	4	Q9BRH3	Q9BRH3 homo sapien
41	149	8.0	1013	4	Q43897	Q43897 homo sapien
42	149	8.0	1013	4	Q9NOS4	Q9NOS4 homo sapien
43	148.5	8.0	414	11	Q9CX06	Q9CX06 mus musculus
44	148.5	8.0	414	11	Q8R4W6	Q8R4W6 mus musculus
45	148	8.0	358	13	Q57434	Q57434 fugu rubrip

ALIGNMENTS

RESULT 1

Q9NRAL ID Q9NRAL PRELIMINARY: PRT: 345 AA.

AC Q9NRAL: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Platelet-derived growth factor C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RX MEDLINE=20268201; PubMed=10806482;

RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M., Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P., Betscholtz C., Heidlin C.-H., Alltalo K., Ostman A., Eriksson U.; PDGF-C is a new protease-activated ligand for the PDGF alpha-1 receptor.

RT Nat. Cell Biol. 2:302-309(2000).

CC - SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL: AF244813; AAF80597.1; -

DR InterPro: IPR000859; CUB_domain.

DR InterPro: IPR000072; PD_growth_factor.

DR Pfam: PF00431; CUB; 1.

DR Pfam: PF00341; PDGF; 1.

DR SMART: SM00042; CUB; 1.

DR SMART: SM00141; PDGF; 1.

DR PROSITE: PS01180; CUB; 1.

DR PROSITE: PS02078; PDGF_2; 1.

SO SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 4; Length 345;

Best Local Similarity 100.0%; Pred. No. 9.5e-170;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSIFGLLVTSALAGQRGTQAEHSNLSKRFSSNKEQNGVDPQHERITVSTNSHS 60

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Db 1 MSFGLLVTSALAGORGTQAEESNLSSKFOFSSNKEDQNGVODPHRITITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLVRLVAEENWVIOITPDERGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||||
Db 61 PRPHYTPRNTVLVRLVAEENWVIOITPDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRWCGSGTVPEKQISKQNOIRIRFVSDEYFPSEPGFCIHNYIMPOFTEAVSPVLPSSA 180
    |||||||
Db 121 GRWCGSGTVPEKQISKQNOIRIRFVSDEYFPSEPGFCIHNYIMPOFTEAVSPVLPSSA 180
QY 181 LPDLNNATAFSTLEDLIRYLEPERMOLDLEDLYRPTWQLGKAFVFGKRSVVDNL 240
    |||||||
Db 181 LPDLNNATAFSTLEDLIRYLEPERMOLDLEDLYRPTWQLGKAFVFGKRSVVDNL 240
QY 241 LEEVRLYSCPTPRNFVSIREELKRTDTIPWGCCLVYKRCGCNACCLHNCNECQVPSK 300
    |||||||
Db 241 LEEVRLYSCPTPRNFVSIREELKRTDTIPWGCCLVYKRCGCNACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLHKSITDVALHEHHECDVCRCSTGG 345
    |||||||
Db 301 VTKKYHEVLQLRPKTVGVLHKSITDVALHEHHECDVCRCSTGG 345

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RESULT 2

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ID 090Y22 PRELIMINARY; PRT; 345 AA.
AC 090Y22;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
GN HSCDGF OR PDGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=UTERUS;
RA Tsai Y.-J., Lee R.K.-K., Lin S.-P.;
RT "Fallotein, a novel growth factor like gene identified in human uterus.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP TISSUE=UTERUS;
RC TISSUE-BRAIN;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Oi-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=1197552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstra P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a Novel Growth Factor That Binds to PDGF alpha and beta Receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF091434; AAF00049.1; -;
DR EMBL: AB033831; BAB03266.1; -;
DR EMBL: AF260738; AAK51637.1; -;
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00180; CUB; 1.
DR PROSITE: PS01180; CUB; 1.

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DR PROSITE: PS0278; PDGF-2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

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Query Match 99.64; Score 1851; DB 4; Length 345;

Best Local Similarity 99.48; Pred. No. 4.4e-169; Mismatches 0; Gaps 0;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSFGLLVTSALAGORGTQAEESNLSSKFOFSSNKEDQNGVODPHRITITVSTNGSIHS 60
    |||||||
Db 1 MSFGLLVTSALAGORGTQAEESNLSSKFOFSSNKEDQNGVODPHRITITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLVRLVAEENWVIOITPDERGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||||
Db 61 PRPHYTPRNTVLVRLVAEENWVIOITPDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRWCGSGTVPEKQISKQNOIRIRFVSDEYFPSEPGFCIHNYIMPOFTEAVSPVLPSSA 180
    |||||||
Db 121 GRWCGSGTVPEKQISKQNOIRIRFVSDEYFPSEPGFCIHNYIMPOFTEAVSPVLPSSA 180
QY 181 LPDLNNATAFSTLEDLIRYLEPERMOLDLEDLYRPTWQLGKAFVFGKRSVVDNL 240
    |||||||
Db 181 LPDLNNATAFSTLEDLIRYLEPERMOLDLEDLYRPTWQLGKAFVFGKRSVVDNL 240
QY 241 LEEVRLYSCPTPRNFVSIREELKRTDTIPWGCCLVYKRCGCNACCLHNCNECQVPSK 300
    |||||||
Db 241 LEEVRLYSCPTPRNFVSIREELKRTDTIPWGCCLVYKRCGCNACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGVLHKSITDVALHEHHECDVCRCSTGG 345
    |||||||
Db 301 VTKKYHEVLQLRPKTVGVLHKSITDVALHEHHECDVCRCSTGG 345

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RESULT 3

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ID 090Y71 PRELIMINARY; PRT; 345 AA.
AC 090Y71;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Fallotein (Platelet-derived growth factor C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=OVARY;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallotein from mouse ovary.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF117608; AAF22516.1; -;
DR EMBL: AF264647; AAK58566.1; -;
DR MGD: MGI:1859631; Pdgcfc.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS0278; PDGF-2; 1.
DR SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

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[illegible][illegible]

QY	121	GRMGSGVVPKQIKS	QIIRVSDPEPSEEGFCIHNIYMPQTEAVSPVLPSPA	160
Db	121	GRMGSGVVPKQIKS	KNHITIRVSDPEPSEEGFCIHNIYMPQTEAVSPVLPSPA	160
QY	181	LPDLNNATIAFTLEDLIR	YPEREKQDLEDLIRPTQOLGKAIVFGRKSKVNDYL	240
Db	181	LSLDLNNATIAFTSVEDLE	IRFLPEDRQIDDLSTLYKPTMYLGLKAPLYGRKSKVAVNL	240
QY	241	LTEYKRLTSCIPRNFVS	IREELKRTDTIIPMGCLLYKRCGGNCACCLHNCNECOVPSK	300
Db	241	LKEEYKRLTSCIPRNFVS	IREELKRTDTIIPMGCLLYKRCGGNCACCLHNCNECOVPSK	300
QY	301	VTKKVNEVLDLPRKTVG	AGKLSLTDVALENNESCDVCVSGSTG	345
Db	301	VTKKVNEVLDLPRKTVG	AGKLSLTDVALENNESCDVCVSGSTG	345

[illegible]

Db 241 LKEEVLKCLPTPRNFSVSIREEIKRTDTRFWPGCLLVKRCGNCACCLHNCQCVPRK 300
 QY 301 VTKKYHEVLQLRPKTVGKGLKHSKLTVDVALEHHECCDCVCRSTGG 345
 Db 301 VTKKYHEVLQLRPKTVGKGLKHSKLTVDVALEHHECCDCVCRKNAGG 345

RESULT 6

Q91946

ID Q91946

AC Q91946

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DE 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Spinal cord-derived growth factor.

GN SCDGF

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_Taxid=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WHITE LEGHORN; TISSUE=SPINAL CORD;

RX MEDLINE=20317014; PubMed=10858496;

RA Hamada T., U-Tel K., Miyata Y.;

RT "A novel gene derived from developing spinal cords, SCDGF, is a unique

RT member of the PDGF/VEGF family.";

RT FEBS Lett. 475:97-102(2000).

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AB033829; BAB03265.1; -

DR InterPro; IPR000859; CUB_domain.

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00341; PDGF; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

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DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

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DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

DR PROSITE; PS0278; PDGF_2; 1.

Qy	59	HSRPFPHYPPNNTLVRLVLAVERNWIQTLFDRRCLEDDPDDICKYDVEVVEEPPDGT	118
Db	65	QSPRPMPSPNPNTLLTRLRLH-QENTRIQVDFQDQLEAEANDICXDVEVEDISETS	123
Qy	119	--ILGRMGSGCTVPGKQISKNOIRIRFVSDEYEPSEBGCINHINIMPOFTEAV-----	171
Db	124	TIIRGRMGCKEYVPPRIKSRNOJKITFKSDDTFVAAPGFKIYSL-LDFOPAASETN	182
Qy	172	-----SPSLPSPALPLDLNNAATFSTLEDDLRILEPERMOLDEDLYR	217
Db	183	WESVTSISGVSYNPSVYDPT-LIADLDKKIAEFPTVEDLKYFPMESQDLENNYL	241
Qy	218	PTWOLLKAFYVGRKSRVVDLNLITEEVRLYCTPRNFVSIREELKRTDTIFMPCGLV	277
Db	242	DTPRYRGASY-HDRKSK-VDLDRLNDADAKRYSCTPRMYSNIREELKTLAVVFPRLCY	299
Qy	278	KRCGNCACCLHNCNECQCVPSKATKYHYEYLDLR--KTGVAGLHKSLTVDALHNHEE	334
Db	300	QRCGNCGCCGTVMNRSCSTCNSGKATKYKHYEYLOEPGHIKRRGAKTMALVDIOLDHNR	359
Qy	335	CDVC 339	
Db	360	CDCTC 364	

RESULT 8	
Q9BWV5	
ID Q9BWV5	PRELIMINARY; PRT; 364 AA

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DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Iris-expressed growth factor short form.
GN IGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=IRIS;
RA Mistow G.;
RT "Iris-expressed Growth Factor (IGF)",
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AY027518; AKR20082.1; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR InterPro: IPR000531; Tonb_boxC.
DR Pfam: PF00451; CUB_1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PSS0278; PDGF_2; 1.
DR PROSITE: PSS0430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8BDEA9EAC CRC64;

```

Query Match	39.9%	Score 740.5;	DB 4	Length 364;
Best Local Similarly	43.28%	Pred. No. 1.4e-62;		
Matches 156;	Conservative 61;	Mismatches 113;	Indels 31;	Gaps 9

```
0Y      3 LFGLLVTLSALAGORRGIOAESNLSKFFQSSKNKEONGVODPCHERITITVSTNGSIHSPR 62
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      5 IFVVLLICANFCSCRDTSATFPOSASIALRANLRDLDY--RDEDTIOWKGMYQVSPP 62
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      63 FPHYTPRTVTVLWMLLVANEENVMVLQTLTFDEFGEJDEDDICTKVDFVEVEEPSGT--IL 120
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      63 FPNSYPRNLTLTWRLHS-QENTRIQLVFDNFQGLEAEANDCRDYDFEVEDISTETPIIR 120
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      121 GRMGSGIVPGKOJISKGNQIIRIFVSEVEFPSEPGCIHNINVMPTTEAV----- 171
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      122 GRMCGHKEVEPRIKSRTNQIITFKRSDDYFPAKGGFYIYSYL-LEDIQPAASETNNESV 180
```

[illegible]

RESULT 9	
Q925I7	
ID Q925I7	PRELIMINARY; PRT; 370 AA

01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Platelet-derived growth factor D.
 GN PDGFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=21231380; PubMed=11331882;
 RA Lachocnelle W.J., Jeffers M., McDonald W.F., Chillaikuru R.A.,
 RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
 RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.,
 RT "PDGF D, A Novel Protease-Activated Growth Factor."
 RL Nat. Cell Biol. 3:517-521(2001).
 DR EMBL: AF355583; AAK38839.1; -
 DR MGD: MGI:1919035; Pdfrf.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB. 1.
 DR SMART: SM00141; PDGF. 1.
 DR PROSITE: PS01180; CUB. 1.
 DR PROSITE: PSS0278; PDGF. 2. 1.
 SO SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;

Query Match	39.7%	Score 737.5	DB 11	Length 370
Best Local Similarity	44.0%	Pred. No. 2.8e-62		
Matches 153, Conservative	59	Mismatches 103	Indels 33	Gaps 9

Oy	16	ORQOASNSJSSKRFQFSSNKEONGYOD - POHERLITVSTNGSHSPREPITYRNVLT	74
Dd	26	ORASTKALRNANLR -----KBESHLDLIDYOARENIOVTSNGHVQSPPFPNSIPIRNLILT	80
Oy	75	WRLVAEENVMIOITLFDERFGLEDPEDDICKYDEVEVEEPSDGT - ILGRWCSGTVPgk	132
Dd	81	IWLRS - QEKTRIQTSFDHQFLAEANDICRYDEVEAVEESSSTVVGRMCCHKETIPR	139
Oy	133	QISGNOIRIFVSDEYHPSRPGCIHNINYPQTEV-----SPS	174
Dd	140	ITSRKNOIKITFKSDDFVAPAGFRKIYISFEDEFQPEASSETMNEBSYTSSFSGVSYSPS	199
Oy	175	VLPSPALPDLNNAIATFASTLEDIRILEBERMOQLDEDLEYRPYWOLLKGAFFVGKRSR	234
Dd	200	ITDPt - LTAADALDKVAAFQVEDLTKHFNVNSQMDOLENIYDTPIPHYGRSTY - HDKSK	257
Oy	235	VVDLMLLTLEVRVLISCTPRNFVSISREBLAKTDITITFWPGCLLVKRCGGANCACCLHCNSEC	294
Dd	258	- VDDIRLNDVDVKRRYSCTPRNHVSIVNIRELKLJTNAVFEPRLCLVAVRGCGNCGCCGVVNMKSC	316

QY 295 QCVPSKYTKYHEVLOLRP---KTGVRGLHKSITDVALEHNEECDCVC 339
 DB 317 TCSSGKTKYKHYHEVLFKPEPGHFKRGRKAKMALVDIOLDHNERCJCIC 364

RESULT 10

Q9E0CT1 PRELIMINARY; PRT; 370 AA.
 ID O9E0CT1
 AC O9E0CT1
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Spinal-cord derived growth factor-B.
 GN RSCDGF-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092670; PubMed=11162582;
 RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
 RT Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 RT SCDF/PDGF-C/fallopelin."
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB052170; BAB18920.1;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BE73 CRC64;

Query Match 39.6%; Score 736; DB 11; Length 370;
 Best Local Similarity 45.6%; Pred. No. 3,9e-62;
 Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

QY 37 EQNCGVDP-POHERITVSTNGSIHSPRPHTYPRNTVLMRLVAVENWVITQLTFDERFG 95
 DB 42 ESNLTLTDRDENIRYTGCHGVSPRPNSYPRNLLTLWRLS-OEKTRTQLAFDHOFG 100
 QY 96 LEDEDDICKRDFEVEEPEPSDGT--ILGRMGSGTVPGKQISKNOJRIREFSVSEYEPSE 153
 DB 101 LEEAENDICRDFEVEEEDSVSSSTVVRGRCGKHEIPRITSRTNOLKITQSDDIYFAK 160
 QY 154 PGFCIHNYIV--NPQTEAV-----SPSVLPSPALPDLNLNNAITAFST 195
 DB 161 PGFIYYSFVEDFQPEAASEINMESVTSFSGVSHSPSVW-DSTLVADALDKAIAEDT 219
 QY 196 LEDLIRLPEERQQLDEDLIRPTWOLLGKAFVGRKSRVVDLNLLEVRVLSCTPRNF 255
 DB 220 VEDLTKFNPAWQDLENTLMDIPRYGRSY-HERKSK-VDLRLDDVDRKYSCTPRNH 277
 QY 256 SVSIREELKRTDIFPMGCLIVKRCGNCACCLHNECCQVPSKYTKYHEVLOLRP-- 313
 DB 278 SVNIRELKLINAVFPFRCLLVYRCGNCGLTNMKSCITSSSKYTKYHEVLFKPEPGH 337
 QY 314 -KTGVRGLHKSITDVALEHNEECDCVC 339
 DB 338 FKRGRKAKMALVDIOLDHNERCJCIC 364

RESULT 11

Q9DIL8 PRELIMINARY; PRT; 290 AA.
 ID O9DIL8
 AC O9DIL8
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 1110003109Rik protein.
 GN PDEGD OR 1110003109Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRAIN-C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arawaka T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AK003359; BAB22735.1;
 DR MGD: MGI:1919035; Pdfigd.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 290 AA; 33425 MW; 14214509E6717D4B CRC64;

Query Match 34.7%; Score 645; DB 11; Length 290;
 Best Local Similarity 45.4%; Pred. No. 1,5e-53;
 Matches 128; Conservative 48; Mismatches 80; Indels 26; Gaps 6;

QY 81 EENNWLTQDTERGLEDPPDDICKYDFVEVEPSDGT--ILGRMGSGTVPGKQISKCN 138
 DB 6 QEKTRIQLSFDHOGLEAENDICRDFEVEEVSSTVVRGRCGKHEIPRITSRTN 65
 QY 139 QIRIRFVSDEFSEPGFCIHNYIVNPQTEAV-----SPSVLPSPA 180
 DB 66 QIKTKFSDDYFAKPRFKIYYSFVEDFQPEAASETMWSVTSFSGVSHSISITPT- 124
 QY 181 LPDLNLNNAITAFSTLEDLIRLEPERWQDLEDLIRPTWOLLGKAFVGRKSRVVDLNL 240
 DB 125 LTADALDKTVAEEFTVEDLTKHNPVSMODLENTLIDTPIHYRGRSY-HNRKSK-VDLDR 182
 QY 241 LTBEVRLYSCPRNFVSISIEELKRTDIFPMGCLIVKRCGNCACCLHNECCQVPSK 300
 DB 183 LNDVVKRYSCTPRNHSVNLBEELKLTNAVFPFRCLLVYRCGNCGLTNMKSCITSSGK 242
 QY 301 VTKKYHEVLOLRP---KTGVRGLHKSITDVALEHNEECDCVC 339
 DB 243 TVKKYHEVLFKPEPGHFKRGRKAKMALVDIOLDHNERCJCIC 284

RESULT 12

Q8QFX6 PRELIMINARY; PRT; 923 AA.
 ID Q8QFX6
 AC Q8QFX6
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Neupophilin-1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
 RT "Neupophilin-1 is required for normal vascular development and is a
 RT mediator of VEGF-dependent angiogenesis in zebrafish."
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY064213; AAL40862.1;
 SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

 Query Match 10.3%; Score 190.5; DB 13; Length 923;
 Best Local Similarity 27.6%; Pred. No. 2.6e-09;
 Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;

 QY 5 GLLVTSALAGORRGQARSNLSTKQFSSNKGQNGVDPQHERLITTSNGSIHSRPP 64
 DB 12 GFLIYSAKNDKCGDN-----IRITSANYLTSPGP 43
 QY 65 HYPRTVLWRLVAEENWVQLPDERFGLEDPEDDICKYDVEVEPSD--GTILGR 122
 DB 44 VSYPSQKCIWYTARGPQRILINPNPHDLEDR---CKYDVEVRGSDVNDGLVCK 100
 QY 123 WCGSGVPGKQSKNQIIRVSDYFPSEPGFCIHYNIVP-----OFTAVSPSVL 176
 DB 101 YCGK-TAPSPVSSGNGQLFKFVSD-YETHGAGFSIRYELFKTGPCSRFTS--SSGVI 156
 QY 177 PSALPLDLLNNAITAFSTLEDLIRYLEPERMQDLEDLYRPTWQLGKAFVGRKSRV 235
 DB 157 KSPGPEKFPNNLDCIFMIFAPKMSIIVLEFESFELEPDTQP-----PAGVCFRIDL 209

 RESULT 13
 O60494 PRELIMINARY; PRT: 3623 AA.
 ID 060494
 AC 060494: Q96R09; PRT: 3623 AA.
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Intrinsic factor-B12 receptor precursor (Intrinsic factor-vitamin B12
 DE receptor).
 GN CUBN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97476251; PubMed-9334227;
 RA Birn H., Verroust P.J., Nexø E., Jacobsen C.,
 RA Christensen E.I., Moestrup S.K.;
 RT "Characterization of an epithelial approximately 460-kDa protein that
 RT facilitates endocytosis of intrinsic factor-vitamin B12 and binds
 RT receptor-associated protein."
 RT J. Biol. Chem. 272:26497-26504(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98241400; PubMed-9572993;
 RA Kozyraki R., Kristiansen M., Sijltharoglu A., Hansen C., Jacobsen C.,
 RA Tommerup N., Verroust P.J., Moestrup S.K.;
 RT "The human intrinsic factor-vitamin B12 receptor, cubilin: molecular
 RT characterization and chromosomal mapping of the gene to 10p within the
 RT autosomal recessive megaloblastic anemia (MGA1) region."
 RL Blood 91:3593-3600(1998).
 RN [3]
 RP SEQUENCE OF 130-3623 FROM N.A.
 RA Amthoff M., Brady S., Verroust P.J., Moestrup S.K., Krahe R.;
 RT "The genomic structure of the human CUBN gene encoding cubilin, the

RT Intrinsic factor-vitamin B12 receptor."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 26 CUB DOMAINS.
 DR EMBL; AF034611; AAC82612.1;
 DR EMBL; AF243129; AAK61830.1;
 DR EMBL; AF243083; AAK61830.1; JOINED.
 DR EMBL; AF243084; AAK61830.1; JOINED.
 DR EMBL; AF243085; AAK61830.1; JOINED.
 DR EMBL; AF243086; AAK61830.1; JOINED.
 DR EMBL; AF243087; AAK61830.1; JOINED.
 DR EMBL; AF243088; AAK61830.1; JOINED.
 DR EMBL; AF243089; AAK61830.1; JOINED.
 DR EMBL; AF243090; AAK61830.1; JOINED.
 DR EMBL; AF243091; AAK61830.1; JOINED.
 DR EMBL; AF243092; AAK61830.1; JOINED.
 DR EMBL; AF243093; AAK61830.1; JOINED.
 DR EMBL; AF243094; AAK61830.1; JOINED.
 DR EMBL; AF243095; AAK61830.1; JOINED.
 DR EMBL; AF243096; AAK61830.1; JOINED.
 DR EMBL; AF243097; AAK61830.1; JOINED.
 DR EMBL; AF243098; AAK61830.1; JOINED.
 DR EMBL; AF243099; AAK61830.1; JOINED.
 DR EMBL; AF243100; AAK61830.1; JOINED.
 DR EMBL; AF243101; AAK61830.1; JOINED.
 DR EMBL; AF243102; AAK61830.1; JOINED.
 DR EMBL; AF243103; AAK61830.1; JOINED.
 DR EMBL; AF243104; AAK61830.1; JOINED.
 DR EMBL; AF243105; AAK61830.1; JOINED.
 DR EMBL; AF243106; AAK61830.1; JOINED.
 DR EMBL; AF243107; AAK61830.1; JOINED.
 DR EMBL; AF243108; AAK61830.1; JOINED.
 DR EMBL; AF243109; AAK61830.1; JOINED.
 DR EMBL; AF243110; AAK61830.1; JOINED.
 DR EMBL; AF243111; AAK61830.1; JOINED.
 DR EMBL; AF243112; AAK61830.1; JOINED.
 DR EMBL; AF243113; AAK61830.1; JOINED.
 DR EMBL; AF243114; AAK61830.1; JOINED.
 DR EMBL; AF243115; AAK61830.1; JOINED.
 DR EMBL; AF243116; AAK61830.1; JOINED.
 DR EMBL; AF243117; AAK61830.1; JOINED.
 DR EMBL; AF243118; AAK61830.1; JOINED.
 DR EMBL; AF243119; AAK61830.1; JOINED.
 DR EMBL; AF243120; AAK61830.1; JOINED.
 DR EMBL; AF243121; AAK61830.1; JOINED.
 DR EMBL; AF243122; AAK61830.1; JOINED.
 DR EMBL; AF243123; AAK61830.1; JOINED.
 DR EMBL; AF243124; AAK61830.1; JOINED.
 DR EMBL; AF243125; AAK61830.1; JOINED.
 DR EMBL; AF243126; AAK61830.1; JOINED.
 DR EMBL; AF243127; AAK61830.1; JOINED.
 DR EMBL; AF243128; AAK61830.1; JOINED.
 DR HSSP; P35555; 1EMN.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR Pfam: PF000431; CUB; 27.
 DR Pfam: PF00008; EGF; 5.
 DR SMART; SM00042; CUB; 26.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_like; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01180; CUB; 27.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_4.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; 3.
 KW Calcium binding; EGF-like domain; Glycoprotein; Hydroxylation;
 KW Receptor; Repeat; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 3623 POTENTIAL.
 SQ SEQUENCE 3623 AA; 398991 MW; A91AVCEA5348651 CRC64;
 INTRINSIC FACTOR-B12 RECEPTOR.

```

Query Match          9.8%; Score 183; DB 4; Length 3623;
Best Local Similarity 26.2%; Pred. No. 8.6e-08;
Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

QY 19 GTAESNLSKRFQF-----SSKKEONG-----VDDPQHERITIVTNGSHSPFPFH 65
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 892 GTDIPSPFTSVNYFLVTFVKSSSTENHGFMAKPSADLACGELITTEST-CTIOSPCHPN 950
   || : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 66 TYPRTNYLVRLVAVEENWMIQLTFDERFGLEDDEDDICKYDFEVEPEPSDGTILGKMG 125
   || : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 951 VYRPGICHTHIL-VQNNHILHLMF-ETFHLEHYN--CTNDYLEVYDTDTSETSLGRVCG 1006
   || : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 126 SGVPGQKQSKGNQIRIRFVSDEFFPSPGFCIHYNIV-----MPOFTEAVSPSVLPSP 179
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1007 K-SIPELTSSGNSLMVFTDSDLAYE-GFLINYEALISATACLOQYTDLCGFSTP-- 1062
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 180 ALPDLILNNAITAFSTLEDILRIYEPFRMQLDLEDLYR---PTMQLLKGKAFVFRKRRV 236
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1063 ----NFPNN-----YFNNW-----ECIYRIVRGQLIAVHFTNFSLEBAI 1099
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 237 DLNLTPE-EVR-----LY--SCTPRNFSVSIRELK-RPDTI-----FW 271
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1100 G-NYTFPLEIRDGGYKSPILGIFGYSNLPPTIISHSNKMLKFKSDQIDTRGSGFSAIW 1158
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 272 PGCLLVKRCGNCACCLHNCOCVPSKYTKYHE---VLQLRPKTGVRLHKSJTDVA 328
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1159 DGS--STGCCGN---LTTSSGFTISPNYPMYPYHSECEYMWLKSHTG-SAFELEFRDFH 1211
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 329 LEHHEEC 335
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1212 LEHHPNC 1218

RESULT 14
ID 057658 PRELIMINARY; PRT: 691 AA.
AC 057658;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN BMP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20267865; PubMed=10806368;
RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosler R.N.,
RA Reynolds P.R.;
RT Cloning of the chick BMP1/tolloid cDNA and expression in skeletal
RT tissues.;
RC Gene 248:233-243(2000).
CL -I- SIMILARITY: CONTAINS 3 CUB DOMAINS.
DR EMBL: U75331; AAC02259.1; -
DR HSSP: P00736; IAP0.
DR MEROPS: M12.005; -
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000130; Zn_MTPeptide.
DR Pfam: PF01400; Astacin; 1.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF00008; EGF; 1.
DR PRINTS: PR00480; ASTACIN.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00235; ZMGC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.

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DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 691 AA; 77843 MW; 01245982B8DC8F28 CRC64;

Query Match          9.8%; Score 182; DB 13; Length 691;
Best Local Similarity 38.5%; Pred. No. 1.2e-08;
Matches 50; Conservative 20; Mismatches 48; Indels 12; Gaps 7;

QY 55 NGSINSPRPHITYPRTNYLVRLVAVEENWMIQLTFDERFGLEDDEDDICKYDFEVEE- 113
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 560 NGSISSPGPRDYPNNKHCYWLVAPTQ-YRISLRFD---FFPEEGNDVCYDFEVRSG 615
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 114 -PSDGTILGKMGSGVPGQKQSKGNQIRIRFVSDEFFPSPGFCIHYNVMOFTFVAVS 172
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 616 LTLADSKLHGKFCGGG-LPGAITSQYNNMRVFRFSYNTV-AKRGKAHF--FSEKQOOL 670
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
QY 173 PSVLPSPALP 182
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 671 PPQIPP-ALP 679

RESULT 15
ID 099JM4 PRELIMINARY; PRT: 34 AA.
AC 099JM4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to platelet-derived growth factor, C polypeptide
DE (Fragment).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC006027; AAH06027.1; -
DR MGD: MGI:1859631; Pdgcfc.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 34 AA; 3618 MW; F4AB6A3A414AED9E CRC64;

Query Match          9.7%; Score 180; DB 11; Length 34;
Best Local Similarity 91.2%; Pred. No. 3.3e-10;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 312 RPKTGVRLHKSJLTDVALLEHHEECDCYCRGSTG 345
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :
DB 1 RPKTGVRLHKSJLTDVALLEHHEECDCVCRGNAG 34
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| :

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Search completed: April 29, 2003, 09:08:08
Job time : 59 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:11 ; Search time 15.5 Seconds

(without alignments)
2139.766 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSRLGLLVTSALAGORRGT.....DVALEHHECDVCVCRGTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	742.5	40.0	370	2 JC7591	spinal cord-derive
2	736	38.6	370	2 UC7592	spinal cord-derive
3	183	9.8	3623	2 T09456	intrinsic factor-B
4	181.5	9.8	730	1 BMHUI	procollagen C-endo
5	179.5	9.7	927	1 J00948	A5 antigen precurs
6	176	9.5	707	2 JC2218	procollagen C-endo
7	176	9.5	3623	2 T08618	intrinsic factor-B
8	173	9.3	823	1 A58788	procollagen C-endo
9	169	9.1	986	1 B58788	procollagen C-endo
10	169	9.1	991	2 I49540	procollagen C-endo
11	154	8.3	449	2 A55362	procollagen I C-pr
12	148.5	8.0	1057	1 A39288	dorsal-ventral pat
13	143.5	7.7	686	1 A59271	Ra-reactive factor
14	139.5	7.5	1070	2 T31069	colloid-BMP-1 like
15	138.5	7.5	597	2 S71352	metalloproteinase
16	138	7.4	709	1 C1HURB	complement subcomp
17	137.5	7.4	695	1 I54763	Ra-reactive factor
18	137.5	7.4	1524	2 T30337	polypeptide - Afri
19	133	7.2	1594	2 T30549	hensin - rabbit
20	132	7.1	419	2 S68207	vascular endotheli
21	130.5	7.0	1464	2 S58984	development protei
22	128	6.9	402	2 T30018	procollagen I C-pr
23	127.5	6.9	767	2 T30018	hypothetical prote
24	127.5	6.9	3871	2 T22812	hypothetical prote
25	125	6.7	198	2 J50735	platelet-derived g
26	123.5	6.6	277	2 A41735	hyaluronate-bindin
27	123.5	6.6	579	2 UC7629	membrane-type fir12
28	120.5	6.5	245	1 TVCTSS	platelet-derived g
29	120.5	6.5	275	2 JC6506	tumor necrosis fac

30	118.5	6.4	276	2 A47290	TSG-6 homolog PS4
31	114.5	6.2	148	2 D49530	16k vascular endot
32	114.5	6.2	241	1 PFHUG2	platelet-derived g
33	112.5	6.1	200	2 I51551	platelet-derived g
34	112.5	6.1	215	2 S08220	platelet-derived g
35	112.5	6.1	226	2 I51550	platelet-derived g
36	111.5	6.0	319	2 I51569	platelet-derived g
37	110.5	5.9	2403	2 A59386	UVS.2 protein - Af
38	110	5.9	166	2 JN0248	sanko - human
39	109	5.9	197	2 S25096	platelet-derived g
40	108.5	5.8	226	1 TVMWS	platelet-derived g
41	108	5.8	196	2 A37359	PDGF-related trans
42	104.5	5.6	232	2 A41551	platelet-derived g
43	104	5.6	196	2 B28964	vascular endotheli
44	104	5.6	211	1 PFHUG1	platelet-derived g
45	103	5.5	770	2 D89447	protein F57C12.1 f

ALIGNMENTS

RESULT 1

JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #extl_change 24-Aug-2001
C:Accession: JC7591
R:Hamada, T., Ul-Tel, K., Imaki, J., Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: DDBJ:AB033832
C:Genetics:
A:Gene: scdf-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial g
F:294-308/Region: conserved motif #status predicted

Query Match	40.0%	Score 742.5	DB 2	Length 370
Best Local Similarity	43.6%	Pred. No. 9.5e-57		
Matches 159	Conservative 59	Mismatches 114	Indels 33	Gaps 10
QY	3	LEGLLVTSALAGORRGTQAEINLSKPOFSSN---KEONGVOD-PQHERITVSTGSI 58		
DB	5	IFVYTLICANFSCSDRTSATPOSASIKALNANLNRDESHNLDLYRRDETQVKGNGY 64		
QY	59	HSRFRPHYTPRNTLVLRVLAEEVNWIOITPDERGLEDDPDDICKYDFVEYEDSGT 118		
DB	65	QSRFRPNFSPRNLLITWRILMS-OENRITOLVFNQGLEAEANDICRYDFVEEDISETS 123		
QY	119	--ILGRMGSGTVPKQISGNOIRIRFVSDVEPSPGCHYINVMQFTAV----- 171		
DB	124	TIRGRMGCKHEVPKRTKNOIKITFKSDDYFVAKPGKIIYSL-LEDFQPAASETN 182		
QY	172	-----SPSVLPSPALPLDLNNAATFSTEDLIRVLEPERMQLDELDLYR 217		
DB	183	WESVTSISGVSNPSVTDPT-LIADALDKKIAEFVTDLDLKTFNPEMQDLENNYL 241		
QY	218	PTMQLGKAFFVRKRSKRVVDLNLTEBVLKISCTPRNFSVSIKELKRDITMPGCLV 277		
DB	242	DTPFRYGRSY-HSRKSR-VLDLRLINDAKRYSCTPRYNVIREEELKLANVFFPRCLV 299		
QY	278	KRGGNACCLHNCNEQCVPSVTKYHEVLDLRP---TGVRLGAKSLDVALENHEE 334		
DB	300	QRGGNCGCTVMRSCSTCNSGKTVKKYHEVLOFERGHLRRRAKTMALVDIOLHNER 359		
QY	335	CDVCV 339		

Db 360 CDCIC 364

RESULT 2

spinal cord-derived growth factor-B precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001

C:Accession: J07592

R:Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/
A:Reference number: J07591; MOID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: J07592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-references: DDBJ:AB052170

C:Genetics:

A:Gene: scdgb-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

Query Match 39.6%; Score 736; DB 2; Length 370;

Best local similarity 45.6%; Pred. No. 3.5e-56;

Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

QY 37 EQNGVOD-PQHERITVSTNGSIHSPPPHPTPTLVLRVLAEEENWVLTQTFDERFG 95

Db 42 ESNHLDLYRDEIRIVTGVGHVQSPFNSPRNLLTLRLHS-QKTRIQLAHDHFG 100

QY 96 LEEDPEDICRYDVEVEPEBDGT--ILGRMGSGTVPGKQISKNQIRIRFVSDETPSE 153

Db 101 LEERENDICRYDVEVEPEBDGT--ILGRMGSGTVPGKQISKNQIRIRFVSDETPSE 160

QY 154 PGFCIHNYI--MPQTEAV-----SPVLPSALPLDLNNAITAFST 195

Db 161 PGFKIYTFEDDQPELASINWESYSSFSYSHSPWN-DSTLADALDAIAEFDI 219

QY 196 LEDLIRLEPERMQLDEDLIRPTMQLGKAFVGRKSRVVDLNLTEVRLXSCPTPNN 255

Db 220 VEDLLKFNPMASODDENLMDTPRYGRSY-HERKSK-VDDLRLNDVYKRSCTPRNH 277

QY 256 SVSIRELRTKTDITFMGCLLVKRCGNACCLHNCOCQVSKYKKYHEVQLRP-- 313

Db 278 SVMRLREKLITNAVFFPRCLLVORCGGCGTLNMRKSCITSSGKTYKKYHEVQLRP 337

QY 314 -KTGVRGLHKSITDVALEHHECDVCV 339

Db 338 FKRGRKAKNMAVLDIQLDHHRCDCIC 364

RESULT 3

T09456
intrinsic factor-B12 receptor cubilin precursor - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002

C:Accession: T09456

R:Kozyrak, R.; Kristiansen, M.; Slahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.

Blood 91, 3593-3600, 1998

A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz

ion.

A:Reference number: Z16677; MOID:98241400; PMID:9572993

A:Accession: T09456

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <KOZ>

A:Cross-references: EMBL:AF034611; NID:93929528; PIDN:AAC82612.1; PID:93929529

C:Genetics:

A:Map position: 10p12

C:Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:456-467/Domain: EGF homology <EGF>

Query Match 9.8%; Score 183; DB 2; Length 3623;

Best local similarity 26.2%; Pred. No. 8.3e-07;

Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

QY 19 GTOAESNLSKFOF-----SNKEONG-----VDPQHERITVSTNGSIHSPPPH 65

Db 892 GTDPSPTISYNNLYTVFVKSSSTENHGMKFAEDLACGELLTST-GTIQSPGHPN 950

QY 66 TYPRNTVLVWRVLAEEENWVLTQTFDERFGEDPEDICRYDVEVEPEBDGTILGWC 125

Db 951 VYPRGICWTWHL-VQPNHLILMF-ETFHLEPRYN--CTNDYLEVYDTSETSLGNYCG 1006

QY 126 SGTVPGKQISKNQIRIRFVSDETFPSEPGCIHNYI-----MPQTEAVSPVLP 179

Db 1007 K-STPPELTSSGNSLMVFTDSDLAIE-GFLINVEAISATACLODYTDGLGFTSP-- 1062

QY 180 ALPLDLNNAITAFSTEDLIRLEPERMQLDEDLYR--PTMQLGKAFVGRKSRV 236

Db 1063 ----NFPNN-----YPPNN-----ECIRIVTRIGQLIAFTNLSLEAI 1099

QY 237 DLNLTFE-EVR-----LY--SCTPRNFVSISEELK-RDTLT-----FW 271

Db 1100 G-NYTDPLEIRDGGYKSPGLGIFYGSLNPLPTIISHNLMKFKSDQIDTSGSAYW 1158

QY 272 PGCLLVKRCGNACCLHNCOCQVSKYKKYHE--VLQLRPKYVGLHKSITDVA 328

Db 1159 DGS--STGCCGN-----LTTSSGTFISPNMPYHSHSECCWMLKSSHG-SAFELFPRDH 1211

QY 329 LEHHEEC 335

Db 1212 LEHHPNC 1218

RESULT 4

BMH01
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human

N:Alternate names: bone morphogenic protein 1 (BMP1)

C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C:Accession: A37278; E58788.

R:Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.;

Science 242, 1528-1534, 1998

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MOID:89072730; PMID:3201241

A:Accession: A37278

A:Molecule type: mRNA

A:Residues: 1-730 <MOZ>

A:Cross-references: GB:M22488; NID:9179499; PIDN:AAA51833.1; PID:9179500

C:Genetics:

A:Gene: GDB:BMP1

A:Cross-references: GDB:M25203; OMIM:112264

A:Map position: 8p21-8p21

C:Function:

A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t

C:Superfamily: procollagen C-endopeptidase; asclatin homology; C1r/C1s repeat homology

C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT

F:130-321/Domain: asclatin homology <AST>

F:322-431/Domain: C1r/C1s repeat homology <C1R1>

F:435-544/Domain: C1r/C1s repeat homology <C1R2>

F:551-587/Domain: EGF homology <EGF>

F:591-700/Domain: C1r/C1s repeat homology <C1R3>

F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644

F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted

F:214/Active site: Glu #status predicted

F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.8%; Score 181.5; DB 1; Length 730;

Best Local Similarity 37.3%; Pred. No. 1.5e-07;

Matches 50; Conservative 20; Mismatches 47; Indels 17; Gaps 7;

QY 55 NSGHSRPHRYPRNTVLVRLVA-VEENWMIQLFDERFGLEDPEDDICKYDEVVEE 113

DB 599 NSGITSFGMKREYPPNKNICMQLVAPQYRISLQDFEETEG-----NDCKYDEVVRS 653

QY 114 --PSDGTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWQFTAEV 171

DB 654 GLTADSKLHGKFGCS-EKPEVITSQYNNMREKSDNTV-SKKGFAHF-----FSEK- 704

QY 172 SPSTLPPSALPLDL 185

DB 705 RPAIQPRGRPHOL 718

RESULT 5

J00048

A5 antigen precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: J00466; J00948

R:Takegi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 295-307, 1991

A>Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology

A:Reference number: J00466; M01D:91337458; PMID:1908252

A:Accession: J00466

A:Molecule type: mRNA

A:Residues: 1-927 <TAK>

A:Cross-references: GB:D10467; GB:D01077; NID:9222962; PIDN:BA01260.1; PID:9222963

A:Experimental source: tadpole, brain

A:Note: this protein has motifs homologous to complement components C1r and C1s and to C

C:comment: This protein is a neuronal cell surface molecule involved in the neuronal rec

C:superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal

C:keywords: duplication; glycoprotein; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-927/Product: A5 antigen #status predicted <A5A>

F:77-138/Domain: C1r/C1s repeat homology <C1R1>

F:147-262/Domain: C1r/C1s repeat homology <C1R2>

F:274-424/Domain: discoidin I amino-terminal homology <DN1>

F:430-584/Domain: discoidin I amino-terminal homology <DN2>

F:646-812/Domain: MAM homology <MAM>

F:861-883/Domain: transmembrane #status predicted <TM>

F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.7%; Score 179.5; DB 1; Length 927;

Best Local Similarity 31.6%; Pred. No. 2.9e-07;

Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

QY 50 ITYSTNSHSRPHRYPRNTVLVRLVA-VEENWMIQLFDERFGLEDPEDDICKYDEV 109

DB 31 IKTISPSYLTSAGYPSHPYSQRCWEMIQAPDEHYORIMNFNFHDEDERE---CKDYV 87

QY 110 EV--EESPDSTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWMP-- 165

DB 88 EVIDGDANQQLGKTYGK-IAPSPLVSTGPSFIRFVSDEYFPG-AGSFIRFVEFTGCP 145

QY 166 ----QFTEA--VSPSVLPSPALPLDLNNAITAFSTLEDIRYLEPPERMQDLE 213

DB 146 ECSRNFSSNGVTSKPKYPEKYPNALECYTIIPAPKMOELV--LEFSEFLEAD 197

RESULT 6

JC2218

procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)

N:Alternate names: bone morphogenic protein 1

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999

C:Accession: JC2218

R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.

Gene 134, 257-261, 1993

A>Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic pr

A:Reference number: JC2218; M01D:94085787; PMID:8262384

A:Accession: JC2218

A:Molecule type: mRNA

A:Residues: 1-707 <MAE>

A:Cross-references: GB:I12249; NID:9406540; PIDN:AAA16313.1; PID:9406541

A:Comment: This protein induces ectopic cartilage formation in vivo.

C:Superfamily: procollagen C-endopeptidase; asparagin homology; C1r/C1s repeat homology

C:keywords: beta-hydroxyasparagine, glycoprotein; hydrolase; metalloproteinase; zinc

F:93-284/Domain: asparagin homology <AST>

F:285-397/Region: complement Ir/Is-like repeat

F:398-510/Region: complement Ir/Is-like repeat

F:398-507/Domain: complement Ir/Is-like repeat

F:514-550/Domain: EGF homology <EGF>

F:554-666/Region: complement Ir/Is-like repeat

F:554-663/Domain: complement Ir/Is-like repeat

F:62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted

F:177/Active site: Glu #status predicted

F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.5%; Score 176; DB 2; Length 707;

Best Local Similarity 43.3%; Pred. No. 4.2e-07;

Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NSGHSRPHRYPRNTVLVRLVA-VEENWMIQLFDERFGLEDPEDDICKYDEVVEE- 113

DB 562 NSGITSFGMKREYPPNKNICMQLVAPQYRISLQDFEETEG---FTEGNDCKYDEVVEVRS 617

QY 114 --PSDGTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEPGF 156

DB 618 LTDSKRLHGKFGCS-ELPATTISQYNNMREKSDNTV-SKKG 659

RESULT 7

T08618

Intrinsic factor-B12 receptor CUBILIN precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002

C:Accession: T08618

R:Moestrup, S.K.; Kozlowski, R.; Kristiansen, M.; Kaye, J.H.; Rasmussen, H.H.; Braul

J. Biol. Chem. 273, 5235-5242, 1998

A>Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibody

A:Reference number: Z16459; M01D:98148073; PMID:9478979

A:Accession: T08618

A:Molecule type: mRNA

A:Cross-references: EMBL:AF022247; NID:93834379; PIDN:AC71661.1; PID:93834380

C:Genetics:

C:Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology

C:keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membra

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>

F:133-164/Domain: EGF homology <EGF1>

F:436-467/Domain: EGF homology <EGF2>

Query Match 9.5%; Score 176; DB 2; Length 3623;

Best Local Similarity 25.5%; Pred. No. 3.4e-06;

Matches 95; Conservative 52; Mismatches 133; Indels 92; Gaps 24;

QY 2 SLFGLLVY--SALAGRGTOAESNLSSKFPSSKEONGVODPOHERITVSTNGSH 59

DB 901 SYVNILYVTFVFKSSSMENRGFTA-----KSSDKLECG-----EVLTAFT--GIIE 944

QY 60 SPFPHRYPRNTVLVRLVA-VEENWMIQLFDERFGLEDPEDDICKYDEVVEE- 119

DB 945 SPHPHRYPRNTVLVRLVA-VEENWMIQLFDERFGLEDPEDDICKYDEVVEE- 119

QY 120 LGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEPGFCIHY-----NIVWQFTAEVSP 173

Db	1001	IGRYCGK-SIPSTLSNNSIKLIFVDSALAHK-GFSINTEAIDASSVCLDYIDNCGM	1058
Qy	174	SVLP--PSALPDL-----LNNAI--TASTIED-----LIRYLEPERQDLE	213
Db	1059	LSSPFPNNYFPPNMECIYRITGVGLNQALHPTD--TLEDYFGSOQVDFE-----IR	1110
Qy	214	DLYRPYDGLGKAFVFGKRSRYVDLNLLEEVRL-----SCPRNFSYSIREELRT	266
Db	1111	DGGYTSPLVG--LY--CGSVLPPTIISHSNKTLKFKSDALATAKGFSK-----	1156
Qy	267	DTIFPQGLILYRGCGNACCLHNCNEQCVSKVTAKYHE--VLDLRPTGVKGLHKS	323
Db	1157	---YWDGS--SRGCGGN---LTTPTGVLTSPNYPMPYHSHSECCWRLEASHG-SPEELE	1206
Qy	324	LTDVALLENHNEEC	335
Db	1207	FQDFHLEHNPSC	1218

RESULT 8

procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
 Alternaten names: bone morphogenic protein splice form BMP-1/HIS
 C:Species: Homo sapiens (man)
 C:Date: 28-Mar-1998 #sequence, revision 09-Apr-1998 #text_change 18-Jun-1999
 C:Accession: A37278; AS8788
 R:Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1998
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-702, 'EKRALPPRRGPHOLKRRVQRNRRTPO' <WOZ>
 A:Cross-references: GB:M2248; NID:9179499; PIDN:AA51833.1; PID:9179500
 R: Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (mTld) are encod
 A:Reference number: A58788; MUID:95096114; PMID:7798260
 A:Accession: A58788
 A:Molecule type: mRNA
 A:Residues: 703-823 <IMK>
 A:Cross-references: GB:L35578; NID:9619423; PIDN:AAAC1703.1; PID:9619424
 C:Genetics:
 A:Gene: GDB:BMP1; BMP-1
 A:Cross-references: GDB:125203; OMIM:112264
 A:Map position: 8p21-8p21
 C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; B
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:328-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
 F:130-321/Domain: astacin homology <ST>
 F:322-431/Domain: C1r/C1s repeat homology <C1R1>
 F:435-544/Domain: C1r/C1s repeat homology <C1R2>
 F:551-587/Domain: EGF homology <EGF>
 F:591-700/Domain: C1r/C1s repeat homology <C1R3>
 F:738-752/Region: histidine-rich
 F:91, 142, 332, 363, 599/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:163-319, 185-205, 322-348, 375-397, 435-461, 488-510, 551-563, 559-572, 574-587, 591-617, 644-66
 F:213, 217, 223, 272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:214/Active site: Glu #status predicted
 F:565/Modified site:erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.3%; Score 173; DB 1; Length 823;
Best Local Similarity 35.6%; Pred. No. 9.3e-07;
Matches 52; Conservative 19; Mismatches 49; Indels 26; Gaps 7;

```

Qy 55 NGSIHSRPREPTTYPRNTVLVWRLVA-VEENWVIOITFDERFGLDEPDIEDCKYDFVEVEE 113
      ||| ||| : ||| : : ||| : : ||| |||
Db 599 NGSIISPGWPREYPPNNKNCIMQVLVAPLQYRISLQDFFEIEG-----NDVCKYDFVEVRS 653

```

[illegible]

RESULT 9

Procollagen Cndopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
 M.ALternate names: bone morphogenic protein 1, tolloid-like splice form
 C.Species: Homo sapiens (man)
 C.Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
 C.Accession: A37278; B58788
 R.Money: J.M.; Rosen, V.; Celeste, A.J.; Mltsoos, L.M.; Whittles, M.J.; Kriz, R.W.;
 Science 242, 1528-1534, 1988
 A.Title: Novel regulators of bone formation: molecular clones and activities.
 A.Reference number: A37278; MUID:89072730; PMID:3201241
 A.Accession: A37278
 A.Molecule type: mRNA
 A.Residues: 1-702, 'EKRPALQPRGRPHQLKRFVQKRNRPQ' <NOZ>
 A.Cross-references: GB:M2248; NID:q179499; PIDN:AAA5183.1; PID:q179500
 R.Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J.Biol.Chem. 269, 32572-32578, 1994
 A.Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are en
 A.Reference number: A58788; MUID:95096114; PMID:7798260

A: Molecule type: mRNA
A: Residues: 703-986 <TAk>
A: Cross-references: GB:J35279; NID:g619860; PIDN:AAC41710.1; PID:g619861

A:Gene: GDB:BMPI; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21

A:Description: intracellular hydrolysis of the carboxyl-terminal propeptide of collagen type I; C:Superfamily: procollagen C-endopeptidase; ascarin C homology; C1/C1s repeat homology; C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F:1-32/Domain: signal sequence; #status predicted <IG> F:23-966/Product: procollagen C-endopeptidase collagen-like splice form #status predicted F:130-321/Domain: ascarin homology <AST> F:322-431/Domain: C1r/C1s repeat homology <C1R1> F:435-544/Domain: C1r/C1s repeat homology <C1R2> F:551-587/Domain: EGF homology <EG1> F:591-700/Domain: C1r/C1s repeat homology <C1R3> F:707-742/Domain: EGF homology <EG2> F:747-856/Domain: C1r/C1s repeat homology <C1R4> F:860-973/Domain: C1r/C1s repeat homology <C1R5> F:911-142-339-353-599/Binding site: carboxylate (Asn) (covalent) #status predicted F:163-319-185-205-322-348-375-387-435-461-488-510-551-563-555-572-574-587-591-617-644 F:213-217-223-272/Binding site: zinc (His, His, His, Tyr) #status predicted F:214/Active site: Glu #status predicted F:565-720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match	9.18;	Score 169;	DB 1;	Length 986;
Best Local Similarity	39.48;	Pred. No. 2.6e-06;		
Matches 43;	Conservative 17;	Mismatches 39;	Indels	

Qy 55 NGSIHSPREPHTYPRNTVLVWRIVA-VEENVWVQLTFDERFGLDEPDEDICKYDFVEVEE 113
 ||||| : | | | : |||| : : | | | | : |||||
 Db 599 NGSITSPPGWREYPPKNCIMQLVAPTOYRISLDFEFEEEG-----NDVCKYDFVEVRS 653

```
QY 114 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRPVSDEYFPSEPGECHY 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 654 GLTADSKLHGKFCGS -EKPEVITSQYNNMRVERKSDNTV-SKKGFAHF 700
```

RESULT 10
149540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse

C;Species: Mus musculus (house mouse)

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TAK>
A:Cross-references: GB:I.33799; NID:g642907; PIDN:AAA61949..1; PID:g642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Superfamily: Clr/Cls repeat homology
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: Clr/Cls repeat homology <CLR1>
F:159-270/Domain: Clr/Cls repeat homology <CLR2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,433/Binding site: carbonylate (Asn) (covalent) #status predicted

A:Residues: 1-686 <JEN>
A:Molecule type: mRNA
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Accession: X02211
A:Cross-references: GI:Y0926; PIDN:CAA71059.1; PID:g4007622
A:Experimental source: tissue liver
A:Note: submitted to GenBank, December 1996
A:Note: parts of this sequence, including the amino end of the mature protein, were d
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500

for

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:58:01 ; Search time 9 Seconds

(without alignments)
1589.926 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSLFGLLVTSALAGQRGT.....DVALEHHECDVCRCSTGTG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179.5	9.7	928	NRPI_XENLA	P28824 xenopus lae
2	176	9.5	707	BMP1_XENLA	P98070 xenopus lae
3	173.5	9.3	616	SPAN_STRPU	P98068 strongyloce
4	169	9.1	986	BMP1_HUMAN	P13497 homo sapien
5	169	9.1	991	BMP1_MOUSE	P98063 mus musculu
6	164.5	8.9	931	NRP2_HUMAN	O60462 homo sapien
7	163.5	8.8	922	NRP1_RAT	O99499 rattus norv
8	163	8.8	925	NRP2_RAT	O35276 rattus norv
9	162.5	8.7	926	VEGD_RAT	O35251 rattus norv
10	160.5	8.6	923	NRP1_MOUSE	P97333 mus musculu
11	160.5	8.6	931	NRP2_MOUSE	O57460 brachydanio
12	159	8.6	1022	TLD_BRARE	O14786 homo sapien
13	158.5	8.5	923	NRP1_HUMAN	P79795 gallus gall
14	157	8.4	914	NRPI_CHICK	O15113 homo sapien
15	154	8.3	449	PCOI_HUMAN	P25723 drosophila
16	148.5	8.0	1057	TLD_DROME	O43815 homo sapien
17	147	7.9	354	VEGD_HUMAN	O00187 homo sapien
18	143.5	7.7	686	MAS2_HUMAN	P97946 mus musculu
19	140	7.5	358	VEGD_MOUSE	P42674 paracentrot
20	139.5	7.5	597	BP10_PARLI	P98064 mus musculu
21	138.5	7.4	639	CRAR_MOUSE	P98066 mus musculu
22	138	7.4	705	BMPH_STRPU	P98065 strongyloce
23	138	7.4	705	CLR_HUMAN	P00736 homo sapien
24	137.5	7.4	699	CRAR_HUMAN	P48740 h complemen
25	132	7.1	419	VEGC_HUMAN	O61398 mus musculu
26	128	6.9	468	PCOI_MOUSE	O08628 rattus norv
27	128	6.9	468	PCOI_RAT	P34007 oryctolagus
28	125	6.7	213	PDGA_RABIT	P97953 mus musculu
29	125	6.7	415	VEGC_MOUSE	P98066 homo sapien
30	123.5	6.6	277	TS6G_HUMAN	P12919 felis silve
31	120.5	6.5	245	PDGB_FELCA	O08859 mus musculu
32	120.5	6.5	275	TS6G_MOUSE	P98065 oryctolagus
33	118.5	6.4	276	TS6G_RABIT	

ALIGNMENTS

RESULT 1	ID	NRPI_XENLA	STANDARD:	PRT:	928 AA.
AC	P28824:				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Neuropilin-1 precursor (A5 protein) (A5 antigen).				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=91337458; PubMed=1908252;				
RA	Takagi S., Hirata T., Agata K., Mochi M., Eguchi G., Fujisawa H.;				
RT	"The A5 antigen, a candidate for the neuronal recognition molecule,				
RL	has homologues to complement components and coagulation factors.";				
CC	Neuron 7:295-307(1991).				
CC	- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE				
CC	CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF				
CC	CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS				
CC	SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY				
CC	SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION				
CC	BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.				
CC	- TISSUE/CELLULAR LOCATION: Type I membrane protein.				
CC	- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER				
CC	NEURONS.				
CC	- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.				
CC	- SIMILARITY: CONTAINS 2 CUB DOMAINS.				
CC	- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.				
CC	- SIMILARITY: CONTAINS 1 MAM DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: D10467; BAA01260.1; -				P52585 orf virus (
DR	HSSP: P12259; 1C2F.				P01127 homo sapien
DR	InterPro: IPR000859; CUB_domain.				P13698 xenopus lae
DR	InterPro: IPR000421; FA5B_C.				P42664 xenopus lae
DR	InterPro: IPR000998; MAM_domain.				P28576 rattus norv
DR	Pfam: PF00431; CUB; 2.				P01128 simian sarc
DR	Pfam: PF00629; MAM; 1.				P49765 homo sapien
DR	Pfam: PF00754; F5_F8_type_C; 2.				P15692 homo sapien
DR	PRINTS: PR00020; MAMDOMAIN.				P04085 homo sapien
DR	SMART: SM00042; CUB; 2.				P52584 orf virus (
DR	SMART: SM00231; FA5B_C; 2.				
DR	SMART: SM00137; MAM; 1.				
DR	PROSITE: PS00740; MAM_1; 1.				

DR	PROSITE: PS01180; CUB; 2.	
DR	PROSITE: PS01285; FA58c_1; 2.	
DR	PROSITE: PS01286; FA58c_2; 2.	
DR	PROSITE: PS50060; MAM_2; 1.	
KW	transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;	
KW	Antigen.	
FT	SIGNAL	1 21
FT	CHAIN	22 928
FT	DOMAIN	22 860
FT	TRANSMEM	861 883
FT	DOMAIN	884 928
FT	DOMAIN	27 141
FT	DOMAIN	147 265
FT	DOMAIN	275 424
FT	DOMAIN	431 584
FT	DOMAIN	646 812
FT	DISULFID	27 54
FT	DISULFID	82 104
FT	DISULFID	147 173
FT	DISULFID	206 228
FT	DISULFID	275 524
FT	DISULFID	431 584
FT	CARBOHYD	150 150
FT	CARBOHYD	261 261
FT	CARBOHYD	300 300
FT	CARBOHYD	523 523
FT	CARBOHYD	844 844
FT	SEQUENCE	928 AA; 103416 MW; AF6323B0A/C789D CR064;

Query Match	9.7%	Score 179.5;	DB 1;	Length 928;
Best Local Similarity	31.6%	Pred. No. 1.4e-07;		
Matches	55;	Conservative	29;	Mismatches 73;
			Indels	17;
			Gaps	7;

```

0Y  ITVANSGISHPRPHEPTVPRATVTLWNRVVAEENVMWLOTFDEBFGLEDPEDDICXKDFV  109
1  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db  31  IKITSPSYLTAGTAPHSTVPSQRCWMLIQAEHYQRIIMINPHFDLEDRE--CKDYDV  87

0Y  110 EV--EESPDSGITLRMCSGTFVPGKOISKQNGQIRIRFVSDSEPFSEPGFCHNYIMVP--  165
1  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db  88  EVIDGDNNNGOLLGKYGCG--IAPSPVLTSGSITRFDSDIETGCG--AGFSIRYVEVFTGP  145

0Y  166 ----QFTEA--VSPSVLPALPDLLNNATTAARSTDLEDLRLEPERMOWDLE  213
1  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db  146 ECSRNFTHSSNGVITSPKPEKYPNAALECTYITIRAPKQOEIV--LEESFELEAD  197

```

RESUL 2	BMP1_XENLA	STANDARD;	PRT;	707 AA
ID	BMP1_XENLA			
1	000000			

AC P96070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94085787; PubMed=8262384;
RA Meeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT Cloning and expression of cDNA encoding Xenopus laevis bone
RT morphogenetic protein-1 during early embryonic development.";
PL Gene 134:257-261(1993).
CC - FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC - DIFFERENTIAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC - DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC TADPOLES: LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -I- SIMILARITY: CONTAINS 3 CUB DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: L12249; AA16313.1; -
DR HSSP: P00736; IAPQ.
DR MEROPS: M12.005; -
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000130; Zn_MTpeptidse.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF01400; Astacin; 1.
DR PRINTS: PR00480; ASTACIN.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_Ca; 1.
DR SMART: SM00235; Zmc; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01142; EGF_1; FALSE_NEG.

DR PROSITE; PS01187; EGF CA: 1.
KM Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolyase; Protease.
KM Metalloprotease; EGF-like domain; zinc; Calcium; Signal;
KM Chondroectoderm

FT	SIGNAL	?	1	?	POTENTIAL.
FT	PROPER	83			POTENTIAL.
FT	CHAIN	84	707		BONE MORPHOGENETIC PROTEIN 1
FT	DOMAIN	84	284		METALLOPROTEASE.
FT	DOMAIN	205	207		METALLOPROTEASE.
FT	DOMAIN	205	207		METALLOPROTEASE.

FT	263	CUB 1.
FT	397	CUB 2.
FT	509	CUB 3.
FT	510	CEG-LIKE, CALCIUM-BINDING (POTENTIAL)
FT	551	CEG 3.
FT	554	ZINC (CATALYTIC) (BY SIMILARITY).
FT	176	ZINC (CATALYTIC)

FT	ACT_SITE	177	177	BY SIMILARITY.
FT	METAL	180	180	ZINC (CATALYTIC) (BY SIMILARITY)
FT	METAL	186	186	ZINC (CATALYTIC) (BY SIMILARITY)
FT	DISULFID	514	526	BY SIMILARITY.
FT	DISULFID	522	535	BY SIMILARITY.

FT	DISULFID	537	550	BY SIMILARITY,
FT CARBOHYD	62	62	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	105	105	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	295	295	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	326	326	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	562	562	N-LINKED (GLCNAC. . .)	(POTENTIAL)
707 AA:	80673 MW:	1B6980071DC9B8D	CR64:	

Query Match	9.5%	Score 176;	DB 1;	length 707;
Best Local Similarity	43.3%;	Pred. No. 2e+07;		
Matches	45;	Conservative	15;	Mismatches 36;
			Indels	8;
			Gaps	5;

OY 55 NGSIHSPREPHITYRNVLVRLVAEBENWITLPDERGLEDEPDIDCKYDEVEE- 113
D6 562 NGSIINSPMPREPEYPPNNKICMQLVAPPO-YKISLKFPQ--FTEEGNDVCAYDEVVEVRSG 617

OY 114 -PSDQTILGRMGSGTVPGKOISKNOIRIKFYSDXYFSEPERG 156
D6 618 LTDSOKLHGKEGS-ELPAVITTSOYNMKRLEFKSDNTV-SKKGF 659

RESULT 3	
SPAN_STRPU	STANDARD;
ID	SPAN_STRPU
	PRT;
	616 AA

FT	DISULFID	380	402	BY SIMILARITY.
FT <td>DISULFID</td> <td>440</td> <td>466</td> <td>BY SIMILARITY.</td>	DISULFID	440	466	BY SIMILARITY.
FT <td>DISULFID</td> <td>493</td> <td>515</td> <td>BY SIMILARITY.</td>	DISULFID	493	515	BY SIMILARITY.
FT <td>DISULFID</td> <td>556</td> <td>568</td> <td>BY SIMILARITY.</td>	DISULFID	556	568	BY SIMILARITY.
FT <td>DISULFID</td> <td>564</td> <td>577</td> <td>BY SIMILARITY.</td>	DISULFID	564	577	BY SIMILARITY.
FT <td>DISULFID</td> <td>579</td> <td>592</td> <td>BY SIMILARITY.</td>	DISULFID	579	592	BY SIMILARITY.
FT <td>DISULFID</td> <td>596</td> <td>622</td> <td>BY SIMILARITY.</td>	DISULFID	596	622	BY SIMILARITY.
FT <td>DISULFID</td> <td>649</td> <td>671</td> <td>BY SIMILARITY.</td>	DISULFID	649	671	BY SIMILARITY.
FT <td>DISULFID</td> <td>712</td> <td>723</td> <td>BY SIMILARITY.</td>	DISULFID	712	723	BY SIMILARITY.
FT <td>DISULFID</td> <td>719</td> <td>732</td> <td>BY SIMILARITY.</td>	DISULFID	719	732	BY SIMILARITY.
FT <td>DISULFID</td> <td>734</td> <td>747</td> <td>BY SIMILARITY.</td>	DISULFID	734	747	BY SIMILARITY.
FT <td>CARBOHYD</td> <td>96</td> <td>96</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	96	96	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>147</td> <td>147</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	147	147	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>337</td> <td>337</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	337	337	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>368</td> <td>368</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	368	368	N-LINKED (GLCNAC. . .)
FT <td>CARBOHYD</td> <td>604</td> <td>604</td> <td>N-LINKED (GLCNAC. . .)</td>	CARBOHYD	604	604	N-LINKED (GLCNAC. . .)
SO <td>SEQUENCE</td> <td>991 AA;</td> <td>111607 MW;</td> <td>68A1847783A0B9E CRC64;</td>	SEQUENCE	991 AA;	111607 MW;	68A1847783A0B9E CRC64;

Query Match	Best Local Similarity	9.1%;	Score 169;	DB 1;	Length 991;
Matches 43;	Conservative 17;	Mismatches 39;	Indels 10;	Gaps 5;	
QY	55	NGSHSPRPPTTYENTLWRLVA-VEENWIOITFPERGLEDPEEDICKYDEVEE	113		
Db	604	NGSITSPCMPEYEPFPNNKNCIMQVLAAPYRISLQDFEFTG-----NDVCKYDFEVEVS	658		
QY	114	--PSSDILLGRWCGSGTVPGKQISKGNQIRIRFVSDSEFPSEPGCIHY	160		
Db	659	GLTADSKLHGKFCGS-EKPEVITTSQYNNMRYEPKSDNTV-SKKGKRAHF	705		

RESULT 6			
NRP2_HUMAN	STANDARD;	PRT;	931 AA.
AC	060462; 014820; 014821;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).		
GN	NRP2 OR VEGF165R2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).		
RX	MEDLINE=97470888; PubMed=9331348.		
RA	Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;		
RT	"Neuropilin-2, a novel member of the neuropilin family, is a high		
RT	affinity receptor for the semaphorins Sema E and Sema IV but not Sema		
RT	III.";		
RL	Neuron 19:547-559(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM A22).		
RC	TISSUE=Breast;		
RX	MEDLINE=98188099; PubMed=9529250;		
RA	Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.;		
RT	"Neuropilin-1 is expressed by endothelial and tumor cells as an		
RT	isoform-specific receptor for vascular endothelial growth factor.";		
RL	Cell 92:735-745(1998).		
RN	[3]		
RP	CHARACTERIZATION.		
RX	MEDLINE=20309748; PubMed=10748121;		
RA	Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;		
RT	"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid		
RT	form of vascular endothelial growth factor (VEGF) and of placenta		
RT	growth factor-2, but only neuropilin-2 functions as a receptor for		
RT	the 145-amino acid form of VEGF.";		
RL	J. Biol. Chem. 275:18040-18045(2000).		
CC	-1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165		
CC	AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.		
CC	-1- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH		

```

CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A22 (SHOWN HERE), A0 AND A17;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF022859; AAC51788.1; -
DR EMBL: AF022860; AAC51789.1; -
DR EMBL: AF016098; AAC12922.1; -
DR HSSP: P12259; ICZT.
DR Genew: HGNC:8005; NRP2.
DR MIM: 602070; -
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_type_C; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS50060; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neutrone; Signal; Repeat; Receptor;
KW Alternative splicing.
FT SIGNAL 1 20 OR 22 (POTENTIAL).
FT CHAIN 21 931 NEUROPILIN-2.
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 865 889 POTENTIAL.
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DOMAIN 671 674 POLY-SER.
FT DOMAIN 28 35 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPALC 809 813 MISSING (IN ISOFORM A17).
FT VARSPALC 809 830 MISSING (IN ISOFORM A0).
FT CONFLICT 602 602 E -> K (IN REF. 1).
SQ SEQUENCE 931 AA; 104830 MW; 270CBAE69A0A797C CRC64;
Query Match 8.9%; Score 164.5; DB 1; Length 931;
Best Local Similarity 29.9%; Pred. No. 2.8e-06;
Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;

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DB 43 PGYODYPHONCENMIYAPPEPNOKIYVNFPHPEIEKHD---CKYDIEIRODSESAD 99
QY 119 ILGMCSGTYPGQOISKNGNRIIRPVSDEFPSPFCIHNYI 162
DB 100 ILGRHCGN-IAPPTLISSGSMYTKFTSD-YAROGAGFSLKYEI 141
RESULT 7
NRPL_RAT STANDARD; PRT; 922 AA.
ID NRPL_RAT
AC Q9QWU9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
DE receptor).
GN NRPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.
RT "Neuropilin is a semaphorin III receptor."
RL Cell 90:753-762(1997).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOREGIST OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF016296; AAC53337.1; -
DR HSSP: P12259; ICZT.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR001092; HLH_basic.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_type_C; 2.
DR PRINTS: PR00020; MAMDOMAIN.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS50060; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neutrone; Signal; Repeat; Receptor.
FT SIGNAL 1 21 POTENTIAL.

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FT CHAIN 22 922 NEUROPIILIN-1.
FT DOMAIN 22 855 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 856 880 POTENTIAL.
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD098B0F2E CMC64;

Query Match 8.8%; Score 163.5; DB 1; Length 922;
Best Local Similarity 36.5%; Pred. No. 3.4e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

QY 50 ITVSTNGSIHSPREPHYRNTVLVRLVAVEENWVIOITPDEREGLEDPEDDICKYDEV 109
DB 31 IRIENPGYITSPGYSTHPSKCEKWLIOAPEYORIMNFNFPLEDRD---CKYDYV 87
QY 110 EV-EEPSDGTILGRWCGSGTVPGKQISKNOIRIRFVSDYFPPSPGCIHYNI 162
DB 88 EVIDGENEGRLMKCKCK-IPAPVYSSGPFILFIKFSVD-YETHAGGSIREI 140

RESULT 8
NR2_RAT STANDARD; PRT; 925 AA.
AC 035276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Neupilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neupilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -I- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOMERS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
LINING IN THE RIBS.
CC -I- SIMILARITY: BELONGS TO THE NEUROPIILIN FAMILY.
CC -I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -I- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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DB EMBL: AF016297; AAC53338.1; -.
DR HSP; P12259; IC2T.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_type_C; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
FT SIGNAL 1 22
FT CHAIN 23 925
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 859 883 POTENTIAL.
FT DOMAIN 884 925 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CMC64;

Query Match 8.8%; Score 163; DB 1; Length 925;
Best Local Similarity 33.8%; Pred. No. 3.8e-06;
Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;

QY 32 FSSNKQNGVQDPQHERITVSTNGSIHSPREPHYRNTVLVRLVAVEENWVIOITFD 91
DB 15 FSGHKVRS-QDPPCGGRNSKDGAYITSPGYQDYPHQNCEWVYAPENQIVLNFN 73
QY 92 ERFGLEDPEDDICKYDEVFE--EPDGTILGRWCGSGTVPGKQISKNOIRIRFVSDY 149
DB 74 PHEIEIKHD---CKYDFEIRDQDSEADLLGKHGCGN-IAPPTISSGSVLVYIKFTSD-Y 128
QY 150 FSEPEGCIHYNI 162
DB 129 ARQAGFSLRYET 141

RESULT 9
VEGD_RAT STANDARD; PRT; 326 AA.
AC 035251;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
growth factor) (FIGF).
GN FIGF OR VEGFD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor (By similarity).
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC bound by non-covalent interactions (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL: AF014827; AAB66557.1; -
DR HSSP: P15692; IVP.
DR InterPro: IPR004153; CXXC.repeat.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR Pfam: PF03128; CXXC; 1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR Mitogen: Growth factor; Glycoprotein; Signal; Repeat;
KM Cleavage on pair of basic residues; Multigene family.
FT SIGNAL 1 21
FT PROPEP 22 93
FT CHAIN 94 210
FT PROPEP 211 326
FT DOMAIN 227 317
FT REPEAT 227 242
FT REPEAT 263 278
FT REPEAT 282 298
FT REPEAT 306 317
FT DISULFID 116 158
FT DISULFID 147 194
FT DISULFID 151 196
FT DISULFID 141 141
FT DISULFID 150 150
FT CARBOHYD 160 160
FT CARBOHYD 190 190
FT CARBOHYD 292 292
SQ SEQUENCE 326 AA; 37112 MW; 1261AF373596C00 CRC64;

Query Match 8.7%; Score 162.5; DB 1; Length 326;
Best local Similarity 30.0%; Pred. No. 1,1e-06;
Matches 61; Conservative 23; Mismatches 80; Indels 39; Gaps 9;

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QY 263 L-KRTDTIFWPGCLLYKRCGNCACCLHNCNCOGY---PSKVTKYHNYDLRPRKTVR 318
DB 129 LKTTITFFKPPCVNVNFRCG---CC--NEESYMCNNTSYISKLPFLSTV--PLTSV- 180
QY 319 GLHKSLLTVALEHNEHCDCVCRG 341
DB 181 ---PELVVPIKIANHNGCKCLPTG 200

RESULT 10
NR01_MOUSE
ID NR01_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-1 precursor (A5 protein).
GN NR01 OR NRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Embryonic brain;
RX MEDLINE=96353149; PubMed=8748368;
RA Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;
RT Developmentally regulated expression of a cell surface protein,
RT neupilin, in the mouse nervous system";
RL J. Neurobiol. 29:1-17(1996).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D50086; BAA08789.1; -
DR HSSP: P12259; IC2T.
DR MGD: MGI:106206; Nrp.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FAS5_C.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_Type_C; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FAS5C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FAS5C_1; 2.
DR PROSITE: PS01286; FAS5C_2; 2.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS00660; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
FT SIGNAL 1 21

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CC -I - SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -I - SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS
CC -I - SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS
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SQ SEQUENCE 931 AA; 104558 MW;

Query Match 8.6%; Score 160.5; DB 1; Length 931;

RESULT 13
 NRPL_HUMAN STANDARD; PRT; 923 AA.
 AC 014786; 060461;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
 GN NRPL OR NRP OR VEGF165R.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM).
 RX MEDLINE=97433084; PubMed=9288753;
 RA He Z., Tessier-Lavigne M.;
 RT "Neuropilin is a receptor for the axonal chemorepellent semaphorin III."
 RL Cell 90:739-751(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39.
 RC TISSUE=Breast;
 RX MEDLINE=98188099; PubMed=9529250;
 RA Soker S., Takashima S., Miao H.-Q., Klagsbrun M.;
 RT "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."
 RL Cell 92:735-745(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (SOLUBLE/SNRP1 ISOFORM), AND SEQUENCE OF 22-31.
 RC TISSUE=Prostatic adenocarcinoma;
 RX MEDLINE=20183929; PubMed=1068880;
 RA Gagnon M.L., Blelberg D.R., Gschman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.;
 RT "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=20309748; PubMed=10748121;
 RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
 RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF."
 RL J. Biol. Chem. 275:18040-18045(2000).
 CC -1- FUNCTION: THE MEMBRANE-BOUND ISOFORM IS A RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B.
 CC COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS.
 CC -1- FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRP1 ISOFORM IS SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, MEMBRANE-BOUND (SHOWN HERE) AND SOLUBLE/SNRP1 ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART

CC AND PLACENTA; MODERATELY IN LUNG, LIVER, SKELETAL MUSCLE, KIDNEY
 CC AND PANCREAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRP1 ISOFORM IS
 CC FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 F5/F8 TYPE C DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF018956; AAC51759.1; -
 CC EMBL: AF016050; AAC12921.1; -
 CC EMBL: AF145712; AAF44344.1; -
 CC DR HSSP; P12259; 1CZT.
 CC DR Genew; HGNC:8004; NRPL.
 CC MIM; 602069; -
 CC Interpro: IPR000859; CUB_domain.
 CC Interpro: IPR000421; FAS5_C.
 CC Interpro: IPR001092; HLH_basic.
 CC Interpro: IPR000998; MAM_domain.
 CC Pfam: PF00431; CUB; 2.
 CC Pfam: PF00629; MAM; 1.
 CC Pfam: PF00754; F5_F8_type_C; 2.
 CC PRINTS; PR00020; MAMDOMAIN.
 CC SMART; SM00042; CUB; 2.
 CC SMART; SM00231; FAS5C; 2.
 CC DR SMART; SM00137; MAM; 1.
 CC DR PROSITE; PS01180; CUB; 2.
 CC DR PROSITE; PS01285; FAS5C_1; 2.
 CC DR PROSITE; PS01286; FAS5C_2; 2.
 CC DR PROSITE; PS00740; MAM_1; 1.
 CC DR PROSITE; PS00600; MAM_2; 1.
 CC DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
 CC Alternative splicing.
 CC -----
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 923 NEUROPILIN-1.
 CC FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 857 879 POTENTIAL.
 CC FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 27 141 CUB 1.
 CC FT DOMAIN 147 265 CUB 2.
 CC FT DOMAIN 275 424 F5/F8 TYPE C 1.
 CC FT DOMAIN 431 583 F5/F8 TYPE C 2.
 CC FT DOMAIN 645 811 MAM.
 CC FT DISULFID 27 54 PROBABLE.
 CC FT DISULFID 82 104 PROBABLE.
 CC FT DISULFID 147 173 PROBABLE.
 CC FT DISULFID 206 228 PROBABLE.
 CC FT DISULFID 275 424 BY SIMILARITY.
 CC FT DISULFID 431 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT DISULFID 431 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 150 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 642 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 645 923 EFP -> GIK (IN SOLUBLE/SNRP1 ISOFORM).
 CC FT CONFLICT 26 26 MISSING (IN SOLUBLE/SNRP1 ISOFORM).
 CC FT CONFLICT 749 749 K -> E (IN REF. 1).
 CC FT CONFLICT 749 749 D -> H (IN REF. 2).
 CC FT CONFLICT 855 855 E -> D (IN REF. 2).
 CC FT SEQUENCE 923 AA; 103120 MW; ADEADC4A849E5D57 CRC64;
 CC -----
 CC Query Match 8.5%; Score 158.5; DB 1; Length 923;
 CC Best Local Similarity 35.7%; Pred. No. 9.3e-06;
 CC Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;
 CC -----
 CC OY 50 ITVSTGSHSPRPHPTHTYVRLVLAEEVNMQLTFDERFGLDEPDICKYDFV 109

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Db 31 IKIESPGYLSPPGYHSPHSSEKCEMLIQADPYORIMINPHFLEDRD---CKDYV 87
QY 110 EV--EERSDGTILGRMGSGTVPKQISKGNQIRIRVSPSEFSEFGFCHINYI 162
Db 88 EVDGENENGFHFRGKFCGK-IAPPVVSSEGFLEIKFVSD-YETHGAGFSIRVEI 140

RESULT 14
NRPL_CHICK STANDARD: PRT; 914 AA.
ID NRPL_CHICK
AC P79795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
GN NRPL OR NRPL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
RX MEDLINE=95324761; PubMed=7601310;
RA Takagi S., Kasuya Y., Shimizu M., Matsura T., Tsuboi M., Kawakami A.,
RA Fujisawa H.;
RT "Expression of a cell adhesion molecule, neuropilin, in the
RT developing chick nervous system.";
RT Dev. Biol. 170:207-222(1995).
R4 -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOMERISIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOKINE ACTIVITY OF SEMAPHORINS (BY
CC SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
CC PROPERTIES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
CC (LAYERS D AND E OF SCGS). AMACRINE CELLS OF RETINA, NEURITES OF
CC DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
CC BLOOD VESSELS IN THE ENTIRE EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC -----
CC EMBL; DA5416; BAA08256.1; -
CC HSSP; P12259; ICZT.
DR InterPro: IPR000859; CUB domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR000936; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00600; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;

```

```

KW Cell adhesion. 1 18
FT SIGNAL 19 914 POTENTIAL.
FT CHAIN 19 914 NEUROPILIN-1.
FT DOMAIN 20 847 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 848 870 POTENTIAL.
FT DOMAIN 871 914 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 139 CUB 1.
FT DOMAIN 145 263 CUB 2.
FT DOMAIN 273 422 F5/8 TYPE C 1.
FT DOMAIN 429 581 F5/8 TYPE C 2.
FT DOMAIN 636 801 MAM.
FT DISULFID 25 52 PROBABLE.
FT DISULFID 80 102 PROBABLE.
FT DISULFID 145 171 PROBABLE.
FT DISULFID 204 226 PROBABLE.
FT DISULFID 273 422 BY SIMILARITY.
FT DISULFID 429 581 BY SIMILARITY.
SQ SEQUENCE 914 AA; 102480 MW; DD2EEDD6FCBB68C CRC64;

Query Match 8.4%; Score 157; DB 1; Length 914;
Best Local Similarity 29.4%; Pred. No. 1.2e-05;
Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;

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Db 29 IKILSPGYLSPPGYHSPHSSEKCEMLIQADPYORIMINPHFLEDRD---CKDYV 85
QY 110 EV--EERSDGTILGRMGSGTVPKQISKGNQIRIRVSPSEFSEFGFCHINYI--P 165
Db 86 EVDIGDGAERLWGRKFCGK-IAPPVVSSEGFLEIKFVSD-YETHGAGFSIRVEKRG 143
QY 166 Q---FTEAVSPSYLP--PSALPLDL-----LNMTFTFSTLEDIRYLEPE 206
Db 144 ECSRNFITSSGMIKSPFPPEKYNLSLECTYITAPKMSILLFESE-----LEPD 195

RESULT 15
PCOL_HUMAN STANDARD: PRT; 449 AA.
ID PCOL_HUMAN
AC 015113; 014550;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Binlamnov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.;
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RT J. Biol. Chem. 269:26280-26285(1994).
RN [2]
RP REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL Unpublished observations (FEB-2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hirahara I., Syoutfuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.;
RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RL Cell Struct. Funct. 21:662-662(1996).

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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:36 ; Search time 12.5 Seconds

(without alignments)
812.073 Million cell updates/sec

Title: US-09-818-943-2

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/prodata/1/1aa/FCUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	US-09-457-066-43	Sequence 43, App1
2	1667	90.2	345	US-09-040-220D-2	Sequence 2, App1
3	1667	90.2	345	US-09-457-066-2	Sequence 2, App1
4	1667	90.2	345	US-09-265-686-2	Sequence 2, App1
5	1667	90.2	345	US-09-540-224-5	Sequence 5, App1
6	752	40.7	370	US-09-457-066-37	Sequence 37, App1
7	752	40.7	370	US-09-540-224-2	Sequence 2, App1
8	746.5	40.4	370	US-09-540-224-4	Sequence 4, App1
9	181	9.8	788	US-08-572-225-1	Sequence 1, App1
10	177.5	9.6	730	US-08-872-757-2	Sequence 2, App1
11	175	9.5	101	US-09-374-135-6	Sequence 6, App1
12	172	9.3	922	US-09-116-473-4	Sequence 4, App1
13	169	9.1	923	US-08-936-135-6	Sequence 6, App1
14	168	9.1	986	US-08-872-757-4	Sequence 4, App1
15	165	8.9	1013	US-08-866-650-3	Sequence 3, App1
16	165	8.9	1013	US-09-021-287-3	Sequence 3, App1
17	165	8.9	1013	US-09-240-473-3	Sequence 3, App1
18	162	8.8	591	US-08-991-408-4	Sequence 4, App1
19	162	8.8	591	US-09-432-473-4	Sequence 4, App1
20	162	8.8	1013	US-08-866-650-5	Sequence 5, App1
21	162	8.8	1013	US-09-021-287-5	Sequence 5, App1
22	162	8.8	1013	US-08-991-408-2	Sequence 2, App1
23	162	8.8	1013	US-09-240-473-5	Sequence 5, App1
24	162	8.8	1013	US-09-432-473-2	Sequence 2, App1
25	158	8.5	449	US-08-839-008-2	Sequence 2, App1
26	158	8.5	449	US-08-839-008-9	Sequence 9, App1
27	155.5	8.4	901	US-08-936-135-22	Sequence 22, App1

28	155.5	8.4	906	US-08-936-135-24	Sequence 24, App1
29	155.5	8.4	909	US-08-936-135-8	Sequence 8, App1
30	155.5	8.4	909	US-08-936-135-10	Sequence 10, App1
31	155.5	8.4	909	US-08-936-135-18	Sequence 18, App1
32	155.5	8.4	914	US-08-936-135-12	Sequence 12, App1
33	155.5	8.4	925	US-09-116-473-2	Sequence 2, App1
34	155.5	8.4	926	US-08-936-135-14	Sequence 14, App1
35	155.5	8.4	926	US-08-936-135-20	Sequence 20, App1
36	155.5	8.4	931	US-08-936-135-16	Sequence 16, App1
37	153.5	8.3	415	US-09-032-523-2	Sequence 2, App1
38	143	7.7	103	US-09-374-135-5	Sequence 5, App1
39	136	7.4	325	US-08-915-795-3	Sequence 3, App1
40	136	7.4	354	US-08-915-795-5	Sequence 5, App1
41	135.5	7.3	358	US-08-915-795-8	Sequence 8, App1
42	133.5	7.2	401	US-08-839-008-5	Sequence 5, App1
43	133.5	7.2	468	US-08-839-008-7	Sequence 7, App1
44	133.5	7.2	468	US-09-032-523-8	Sequence 8, App1
45	132	7.1	321	US-08-915-795-9	Sequence 9, App1

ALIGNMENTS

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RESULT 1
US-09-457-066-43
; Sequence 43, Application US/09457066
; Patent No. 6432673
GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-457-066-43

Query Match      100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGLLLTSALAGQRTGTRAESNLSKQLSSDKQNGVDPREHRYVITGNGSIHS 60
        |||||||
DB      1 MLLGLLLTSALAGQRTGTRAESNLSKQLSSDKQNGVDPREHRYVITGNGSIHS 60
        |||||||

QY      61 PKPPHTPRRMVWVLRVAVDENVRIOLPDERFGLEDPPDDICKDFVEEPPSGSVL 120
        |||||||
DB      61 PKPPHTPRRMVWVLRVAVDENVRIOLPDERFGLEDPPDDICKDFVEEPPSGSVL 120
        |||||||

QY      121 GRMGSGTVGKQTSKGNHRIREFVSDPEPSPGFCIHYSIIMPQVETTSVSLPPSS 180
        |||||||
DB      121 GRMGSGTVGKQTSKGNHRIREFVSDPEPSPGFCIHYSIIMPQVETTSVSLPPSS 180
        |||||||

QY      181 LSDDLNNAVTASTELEELIRYLEPPDRMOYDLSLKPWQLGKAFLYGGKSKVNNL 240
        |||||||
DB      181 LSDDLNNAVTASTELEELIRYLEPPDRMOYDLSLKPWQLGKAFLYGGKSKVNNL 240
        |||||||

QY      241 LKEEVLYSTPKNFSYSIREELKRTDTIPWPGCLVYKRGCGACACIHNCCOCVPRK 300
        |||||||
DB      241 LKEEVLYSTPKNFSYSIREELKRTDTIPWPGCLVYKRGCGACACIHNCCOCVPRK 300
        |||||||

QY      301 VTKRYHEVLQLRPKTGKGLHKSITDVALEHHEECDCVCGNAGG 345
        |||||||
```

```

Db          301 VTKRYHEVLQRPRTGVKGLKSLTJVDVALEHHHECCCVCRGNAGG 345

RESULT 2
US-09-040-220D-2
: Sequence 2, Application US/09040220D
: Patent No. 6391311
: GENERAL INFORMATION:
: APPLICANT: Ferrara, Napoleone
: TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
: TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
: TITLE OF INVENTION: PROTEIN I AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
: TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
: FILE REFERENCE: P1122
: CURRENT APPLICATION NUMBER: US/09/040,220D
: CURRENT FILING DATE: 1998-03-17
: NUMBER OF SEQ ID NOS: 8
: SEQ ID NO 2
: LENGTH: 345
: TYPE: PRT
: ORGANISM: Human
: US-09-040-220D-2

```

Query Match	90.28	Score 1667	DB 4	Length 345
Best Local Similarity	87.08	Pred. No. 4.6e-175		
Matches 300	Conservative 27	Mismatches 18	Indels 0	Gaps 0

Qy	1	MLGILLLTALAGORPTGAENSSKLTQSDKRONGVOPRHRVYITGNSIHS	60
Db	1	MSLGLLLLTALAGQOQTOAESNLSKFOFSSNKQNGVODPQHRITITVSTNGSIHS	60
Qy	61	KPEPHYTPRNKVLWRLVAVDENVRIOLTDERFERGLEDPEDDICKYDFVEEESDGSVL	120
Db	61	PRPEHYTPRNVLWRLVAVDENWIOLTDERFERGLEDPEDDICKYDFVEEESDGTIL	120
Qy	121	GRMGSGVPGKQTSKGNHIRFVSDSEYPPSEPGFCIHNSIIMPQVETTSVSPLEPSS	180
Db	121	GRMGSGVPGKQTSKGNQIRIRFVSDSEYPPSEPGFCIHNIYMPQTEAVSVSPLEPSA	180
Qy	181	LSLDLNNAYTAESTLEELIYTERDPKQVODLSLYKPYMQLGKAFLYGKSKSVNVLNL	240
Db	181	LPDLNLNAYTAESTLEELIYTERPKQVODLELYRPTQMLGKAFVPSKSKSVNDLNL	240
Qy	241	LKEEYKLYTSCTPRNFSVISIREELKRTDTIEMPGCLLVKRCGAGNACCLHNCNEQCVPRK	300
Db	241	LTEEYRLYTSCTPRNFSVISIREELKRTDTIEMPGCLLVKRCGAGNACCLHNCNEQCVPSK	300
Qy	301	VTKKYHEVLOLRPTGYVGLKSLTDVALNHNHNECCDVCVSGNMG	345
Db	301	VTKKYHEVLOLRPTGYVGLKSLTDVALNHNHNECCDVCVSGSTG	345

```

RESULT 3
US-09-457-066-2
Sequence 2, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debora G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0.
SEQ ID NO 2
LENGTH: 345

```

```

: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-457-066-2

Query Match          90.2%   Score 1667;   DB 4;   Length 345;
Best Local Similarity 87.0%   Pred. No. 4.6e-175;
Matches 300; Conservative 27;   Mismatches 18;   Indels 0;   Gaps 0;

```

Qy	1	MELGILLTALAGORGTGAENSSKIOJLSDKRONOVOPRHRVYITSGNSIHS	60
Db	1	MSLGLLLLTALAGORGTGAENSSKREFSSNKONGOPQOHERIITVSTNGSIHS	60
Qy	61	PKFPHYPRNMVLMWRYAAYDENRIOTFDERGLEDPEDDICKYUFEVEEPPSDSVL	120
Db	61	PRPHYTPRNVLMWRYAAYDENWIOJTFDERGLEDPEDDICKYUFEVEEPPSDSTIL	120
Qy	121	GRMGSGTVPKQOTSKGNHIRFVSDEYFPESEFGCIHYSIIMQVETETTSVSPVLPSS	180
Db	121	GRMGSGTVPKQOTSKGNQIRFVSDEYFPESEFGCIHYNVMPQTEAVSPVLPSPA	180
Qy	181	LSLDDLNNAYTAFSTLEELRYLEPERDWMQYDULSVKPYMQLGKAFLYUKSKSKVYNL	240
Db	181	LPDLNNAYTAFSTLEELRYLEPERQWDLDEJLYRPTMQLGKAFLVFGKSKSVYDNL	240
Qy	241	LKEEYKILSCIPRNPSVSIREFLKRITDIIMPBGCLLYKRGGNCACCLHNCNECOSVPRK	300
Db	241	LTEEYRILSCIPRNPSVSIREFLKRITDIIMPBGCLLYKRGGNCACCLHNCNECOSVPRK	300
Qy	301	VTKKYUHEVLOLRPKTGVGKILSLTDVALENNECSDCVSGNNGG	345
Db	301	VTKKYUHEVLOLRPKTGVGKILSLTDVALENNECSDCVSGNNGG	345

```

RESULT 4
US-09-265-686-2
: Sequence 2, Application US/09265686
: Patent No. 6455283
: GENERAL INFORMATION:
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Kuo, Sophia S.
: TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
: FILE REFERENCE: P1123P2
: CURRENT APPLICATION NUMBER: US/09/265,686
: CURRENT FILING DATE: 1999-03-10
: PRIOR APPLICATION NUMBER: US 09/040,220
: PRIOR FILING DATE: 1998-03-17
: PRIOR APPLICATION NUMBER: US 09/184,216
: PRIOR FILING DATE: 1998-11-02
: NUMBER OF SEQ ID NOS: 8
: SEQ ID NO 2
: LENGTH: 345
: TYPE: PRT
: ORGANISM: Human
US-09-265-686-2

```

[illegible]

[illegible]

```

RESULT 5
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540, 224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-09-540-224-5

```

RESULT 6
 US-09-457-066-37
 : Sequence 37, Application US/09457066
 : Patent No. 643673
 : GENERAL INFORMATION:
 : APPLICANT: Gao, Zeren
 : APPLICANT: Hart, Charles E.
 : APPLICANT: Piddington, Christopher S
 : APPLICANT: Sheppard, Paul O.
 : APPLICANT: Shoemaker, Kimberly E.
 : APPLICANT: Gilbertson, Debra G.

```

?   APPLICANT: West, James W.
?   TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
?   FILE REFERENCE: 98-60
?   CURRENT APPLICATION NUMBER: US/09/457,066
?   CURRENT FILING DATE: 1999-12-07
?   NUMBER OF SEQ ID NOS: 50
?   SOFTWARE: FastSeq for Windows Version 3.0
?   SEQ ID NO 37
?   LENGTH: 370
?   TYPE: prf
?   ORGANISM: Homo sapiens
?   OS-09-457-066-37

```

```

RESULT 7
US-09-540-224-2
: Sequence 2, Application US/09540224
: Patent No. 6468543
: GENERAL INFORMATION:
: APPLICANT: Gilbertson, Debra G.
: APPLICANT: Hart, Charles E.
: TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
: TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZWEGFA
: FILE REFERENCE: 00-28
: CURRENT APPLICATION NUMBER: US/09/540,224
: CURRENT FILING DATE: 2000-03-31
: EARLIER APPLICATION NUMBER: US 60/180,169
: EARLIER FILING DATE: 2000-02-04
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 370
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-09-540-224-2

```

```

QY 37 EQNQVQD-PRHREVTYVTSNGNSHSPKFPHTHYPRNMVLWRLAVADENVRQTLTFDEREG 95
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 42 ESNHLLTDLXRDEIYQKKGNGYQSPRFPNSYPNNLLTWRHLS-QENTRIQLVFDNQFG 100C
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 96 LEDPEDDICKYDPEVEBPSDGSVL--GRMGSGSTVPGKQTSKGNHLRIKRVSDYEPFSE 155

```

```
Db 101 LEEENDICRDEFEVEDISETSTIIRGRCGHEVEPRIRNQTIFKSDPYAK 160
QY 154 PGFIHISII--MPVETTT-----SPSVLPSSSLDILNNVAFST 195
Db 161 PGFIYISLEDFOPAAASETNMESVTSISGVSNSPSTDP-TLADADKRIAEFT 219
QY 196 LEEIRLEPRDQVDDLSYKPTWLLGKAFLYGKSKVNNLKEEVLYSCTPRNF 255
Db 220 VEDLKATFNESQEDLENWYLDTPRYGRSY -HDKRSK -VDDLRLNDKARYSCTPRN 277
QY 256 SVSIRELKRDTTFWGCCLLYKRCGNCACCLHNCNCCVPRKVTKKIHEVQLRP-- 313
Db 278 SVNIRELKLANNVFFPRCLYORCGCGGCVNMRSCGTCNKGTVKKIHEVQLRP 337
QY 314 -KTGVKGLHKSITDVALEHHECCDVC 339
Db 338 IKRGRAKTMAVDIQLDHERCDJC 364
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```
RESULT 8
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ. ID NOS.: 9
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRP
; ORGANISM: Mus musculus
US-09-540-224-4
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```
Query Match 40.4%; Score 746.5; DB 4; Length 370;
Best Local Similarity 43.5%; Pred. No. 1.3e-73;
Matches 151; Conservative 63; Mismatches 102; Indels 31; Gaps 9;
```

```
QY 16 ORGTBRESNLSKQLQSDKQGVQDPRHERVYITSGNSHSPKFPHTYPRNNVLW 75
Db 26 QRSIKALRNAN---LRDESNHLDLYORENIQVTSNGHVOSPRPNYPRLLLTW 81
QY 76 RLVAVDENVRIQLTFDERFGLDEPEDDICKYDEVEEPSDGS--VLGRMCGSGTVEGKQ 133
Db 82 WLRS-QEKTRIQLSFDHGFGLAEANDICRDFVEVEVSSSTIVVGRMGKHEIPRI 140
QY 134 TSKGNHRIREFVDEYPPSEPGCIHYSII--MPVETTT-----SPSV 175
Db 141 TSPNQIKITFKSDDYFAKRGFKIYSFVEDFQPEAASETNMESVTSFSGVSHSPSI 200
QY 176 LPSSSLDILNNVAFSTLEELIRYLEPRDQVDDLSYKPTWLLGKAFLYGKSKV 235
Db 201 TDP-TLADADKRIAEFTVDFEVLKHFNPVSMODDLENYLDTPHYGRSY -HDKRSK 257
QY 236 VNLLKEEVLYSCTPRNFVSIRELKRDTTFWGCCLLYKRCGNCACCLHNCNCCQ 295
Db 258 VDDLRLNDKARYSCTPRNHSVNIRELKLANNVFFPRCLLYKRCGNCAGGCVNMRSC 317
QY 296 CVPRKVTKKIHEVQLRP---KTGVKGLHKSITDVALEHHECCDVC 339
Db 318 CSSGKTVKKIHEVQLRPFGRGKAKNNALVDIQLDHERCDJC 364
```

```
RESULT 9
US-08-572-225-1
```

```
; Sequence 1, Application US/08572225
; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sierfon, Alexander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halliuh, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-572-225-1
```

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Query Match 9.8%; Score 181; DB 1; Length 788;
Best Local Similarity 42.6%; Pred. No. 8.8e-11;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
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```
QY 55 NGSIHSPKFPHTYPRNNVLRLVAVDENVRIQLTFDERFGLDEPEDDICKYDEVEE- 113
Db 401 NGSIISGMPREYPPNKNCIQWLVAPTQ-YRISLQFD---FFETEGNDVCKYDEVEVRSG 456
QY 114 -PSDGSVLGRMCGSGTYPGKQTSKGNHRIREFVDEYPPSEPGCIHY 160
Db 457 LTLASKLHGRGCS-EKPEVITSOYNNMRVEFKSDNTV-SKRGKAHF 502
```

```
RESULT 10
US-08-872-757-2
; Sequence 2, Application US/08872757
; Patent No. 6258584
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sierfon, Alexander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-757-2

Query Match 9.6%; Score 177.5; DB 4; Length 730;
Best Local Similarity 38.1%; Pred. No. 1.9e-10;
Matches 48; Conservative 18; Mismatches 45; Indels 15; Gaps 6;
QY 55 NGSIHSPKPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
DB 599 NGSIHSPKPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
QY 114 -PSDGSVLGRMGSGTYVGKOTSGKNHRIREFVSDPEFPGFCIHYSIIMPOVETTS 172
DB 655 LTRHSLKLGKFCGS-EKPEVITSOYNNMVEFKSDNTV-SKKGFKAFH-----FSENR 705
QY 173 PSVLP 178
DB 706 PALQP 711

RESULT 11
US-09-374-135-6
Sequence 6, Application US/09374135
Patent No. 6277972
GENERAL INFORMATION:
APPLICANT: Afari, Daniel E.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: BPC-1, A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
FILE REFERENCE: 1703-017. US1
CURRENT APPLICATION NUMBER: US/09/374,135
CURRENT FILING DATE: 1999-08-10
PRIORITY APPLICATION NUMBER: 60/095,982
PRIORITY FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 101
TYPE: PRT
ORGANISM: Mouse
US-09-374-135-6

Query Match 9.5%; Score 175; DB 4; Length 101;
Best Local Similarity 42.1%; Pred. No. 1.5e-11;
Matches 45; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 56 GSIIHSPKPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
DB 1 GSIIHSPKPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
QY 114 PSDGSVLGRMGSGTYVGKOTSGKNHRIREFVSDPEFPGFCIHYSIIMPOVETTS 172
DB 57 TADSKLHKGFCGS-EKPEVITSOYNNMVEFKSDNTV-SKKGFKAFH 101

RESULT 12
US-09-116-473-4
Sequence 4, Application US/09116473
Patent No. 6428965
GENERAL INFORMATION:
APPLICANT: Kolodkin, Alex
APPLICANT: Ginty, David
TITLE OF INVENTION: SEMAPHORIN RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,473
FILING DATE: 17-JUL-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/052,762
FILING DATE: 17-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.74973
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-116-473-4

Query Match 9.3%; Score 172; DB 4; Length 922;
Best Local Similarity 31.5%; Pred. No. 1.1e-09;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
QY 2 LILGLLITSAIGORITRAESNLSSKLLSSDKEDNGVODRHEHNVYISGSIHSP 61
DB 7 LILGLLITSAIGORITRAESNLSSKLLSSDKEDNGVODRHEHNVYISGSIHSP 61
QY 62 KPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE-EPSPGSV 119
DB 43 GYHSPKPHPTPRNNVLYRLVAVDENVRIOITFDERFGLDEPDICKYFVEVEE-EPSPGSV 119
QY 120 LGRMGSGTYVGKOTSGKNHRIREFVSDPEFPGFCIHYSIIM-POVETTS-TPSS 174
DB 100 WGRFCGR-IPSPVSSGPGPLFTKFSVD-YETGAGFSIRYEIKRPGCSQNTVAPT 155

RESULT 13
US-08-936-135-6
Sequence 6, Application US/08936135
Patent No. 6034293
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-135-6

Query Match 9.1%; Score 169; DB 3; Length 923;
Best Local Similarity 31.5%; Pred. No. 2.4e-09;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

QY 2 LLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEONGVQDPRHERVVTISGNGSIHSP 61
DB 7 LLCATLALALAG-----AFRSDKCG-----TKIENGYLTSP 42

QY 62 KPHTYRNWLVWRLVAVDENVRIOITPDERGLEPDEDDICKYDVEV--EPPSGSV 119
DB 43 GYPHSYHPSKCEWLIQAPPEYQIIINFNPHQLEDRD---CKYDVEVIDGENEGRL 99

QY 120 LGRWCGSGYVPGKQTSKGNHRIRFVSDSEYFPPSPGCIHYSITM--POYLET-TSPS 174
DB 100 WGFECGR-IMPSPVSSGPFLLFKFVSD-YETHGAGSIRKELFKRPECQNTAFT 155

RESULT 14
US-08-872-757-4
Sequence 4, Application US/08872757
Patent No. 6258584
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Alexander
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-757-4

Query Match 9.1%; Score 168; DB 4; Length 986;
Best Local Similarity 40.7%; Pred. No. 3.4e-09;
Matches 44; Conservative 16; Mismatches 40; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHYTYRNWLVWRLVAVDENVRIOITPDERGLEPDEDDICKYDVEVEE- 113
DB 599 NGSISRGWPKREYPPNKNQWLAPQO-YRISLQFD---FFTEGNDVCKYDVEVRSRG 654

QY 114 -PSDGSVLGRWCGSGYVPGKQTSKGNHRIRFVSDSEYFPPSPGCIHY 160
DB 655 LTAQSKLHGKFCGS-EKPEVITSOYNNMRYEKRSDNTV-SKKGRKHF 700

RESULT 15
US-08-866-650-3
Sequence 3, Application US/08866650
Patent No. 5939321
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
FILING DATE:

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:57:36 ; Search time 33.5 Seconds
(without alignments)
1372.283 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848
Sequence: 1 MLLGLLLLSALAGQRTGT.....DVALEHHECDCCVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 23: /SIDS2/gcgcdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	21	Mouse zvegf3, SRQ
2	1848	100.0	345	21	Mouse zvegf3, SRQ
3	1848	100.0	345	21	Mouse zvegf3, SRQ
4	1848	100.0	345	22	Mouse zvegf3, SRQ
5	1848	100.0	345	23	Mouse zvegf3, SRQ
6	1848	100.0	345	23	Mouse zvegf3, SRQ
7	1848	100.0	345	20	Human VEGF-E prote
8	1667	90.2	345	20	Human PRO200 prote
9	1667	90.2	345	20	Human vascular end
10	1667	90.2	345	21	Human zvegf3, SRQ

11	1667	90.2	345	21	AA24250
12	1667	90.2	345	21	AA24322
13	1667	90.2	345	21	AA24633
14	1667	90.2	345	21	AA24635
15	1667	90.2	345	21	AA24644
16	1667	90.2	345	21	AA24650
17	1667	90.2	345	21	AA24651
18	1667	90.2	345	21	AA24657
19	1667	90.2	345	21	AA24678
20	1667	90.2	345	21	AA24684
21	1667	90.2	345	21	AA24685
22	1667	90.2	345	21	AA24688
23	1667	90.2	345	21	AA24689
24	1667	90.2	345	22	AA24690
25	1667	90.2	345	22	AA24691
26	1667	90.2	345	22	AA24692
27	1667	90.2	345	22	AA24693
28	1667	90.2	345	22	AA24694
29	1667	90.2	345	22	AA24695
30	1667	90.2	345	22	AA24696
31	1667	90.2	345	22	AA24697
32	1667	90.2	345	22	AA24698
33	1667	90.2	345	23	AA24699
34	1667	90.2	345	23	AA24700
35	1667	90.2	345	23	AA24701
36	1667	90.2	345	21	AA24702
37	1667	90.2	345	21	AA24703
38	1667	90.2	345	23	AA24704
39	1659	89.8	345	21	AA24705
40	1659	89.8	345	21	AA24706
41	1659	89.8	345	21	AA24707
42	1576	85.3	354	21	AA24708
43	1576	85.3	354	21	AA24709
44	1559	84.4	318	21	AA24710
45	1524.5	82.5	339	21	AA24711

ALIGNMENTS

RESULT 1	AA24711	standard; Protein; 345 AA.
ID	AA24711	standard; Protein; 345 AA.
AC	AA24711	standard; Protein; 345 AA.
DT	09-MAR-2001	(first entry)
DE	Mouse zvegf3, SRQ	ID NO:35.
XX	Mouse: zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;	
KW	murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;	
KW	neovascularisation; tissue repair; proliferation; differentiation;	
KW	liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;	
KW	periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;	
XX	immunomodulation; hepatic.	
OS	Mus musculus.	
XX	WO200066736-A1.	
XX	09-NOV-2000.	
XX	03-MAY-2000; 2000MO-US40047.	
XX	03-MAY-1999; 99US-0304216.	
XX	10-NOV-1999; 99US-0164463.	
XX	04-FEB-2000; 2000US-0180169.	
XX	(ZYMO) ZYMOGENETICS INC.	
XX	Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;	
XX		

Query Match	Best Local Similarity	Score	DB	Length
Matches 345; Conservative	100.0%;	1848;	DB 21;	345;
			Mismatches 0;	Indels 0;
			Gaps 0	
Sequence 345 AA:				
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1 MLLGLLTLTLAGORTGRTAESNLSSKLTQLSSDKONGVDPRIHERVTTISGNSIHS				
61 PRFPHPTPRNNMVLWFLVAVDENVRQLTFDERFGLEDDEDDICKDYVEVEEPPSGSVL				
61 PRFPHPTPRNNMVLWFLVAVDENVRQLTFDERFGLEDDEDDICKDYVEVEEPPSGSVL				
121 GWMCGSGTVPGKOTSGNIRIRFVSDSEFPSPGCHYSTIIMPVTEFTSTSVLPSS				
121 GWMCGSGTVPGKOTSGNIRIRFVSDSEFPSPGCHYSTIIMPVTEFTSTSVLPSS				
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181 LSLDLNNNAVTAFTSEELIRYLEPDRMQVDLSLYKPMWLKGAFLYLGKSKSVNLM				
241 LKEEVKLYISCTPRNFSVSIREELKRTDTTFPGCLLVKRGCGNACCLHNCNECQCPVR				
241 LKEEVKLYISCTPRNFSVSIREELKRTDTTFPGCLLVKRGCGNACCLHNCNECQCPVR				
301 VTKKTHEVQLRPRKTGVKGLKSLTDVALEHNEECDCVCRGNAAG				
301 VTKKTHEVQLRPRKTGVKGLKSLTDVALEHNEECDCVCRGNAAG				

AC AAY96861;
 DT 26-SEP-2000 (first entry)
 DE Murine vascular endothelial growth factor homologue, ZVEGF3.
 KM Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
 KM Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
 KM chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;
 KM anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
 KM vulary.
 OS Mus musculus.
 XX WO200034474-A2.
 XX
 XX PN 15-JUN-2000.
 XX PD
 XX PF 07-DEC-1999; 99WO-US28968.
 XX PR 07-DEC-1998; 98US-0207120.
 XX PR 06-JUL-1999; 99US-0142576.
 XX PR 21-OCT-1999; 99US-0161653.
 XX PR 12-NOV-1999; 99US-0165255.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 XX WPI: 2000-423420/36.
 DR .N-PSDB: AAA51527.
 PT Novel zvegf3 polypeptides and nucleotides encoding them useful for
 PT stimulating growth of smooth muscle cells and fibroblasts comprising an
 PT epitope bearing portion of a specific amino acid sequence
 XX
 XX Claim 1; Page 169-170; 173pp; English.
 XX
 XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor
 CC homologue. Polypeptides comprising an epitope-bearing portion human or
 CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor
 CC domain and a CUB domain (generic sequence motifs are shown in AAY96859
 CC and AAY96860). The growth factor domain is characterized by an
 CC arrangement of cysteine residues and beta-strands that is characteristic
 CC of the "cysteine knot" structure of the platelet-derived growth factor
 CC (PDGF) family. The CUB domain shows homology to CUB domains in
 CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
 CC protein, bovine acidic seminal fluid protein and Xenopus laevis
 CC tollloid-like protein. Structural analysis and homology predict that
 CC ZVEGF3-like peptides complex with a second polypeptide to form multimeric
 CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.
 CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
 CC muscles cells; for activating cell surface PDGF-alpha receptor and for
 CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
 CC useful for regulating (post-development) organ growth, regeneration and
 CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
 CC antagonists are useful for treating cancer, rheumatoid arthritis,
 CC diabetic retinopathy, ischemic limb disease, peripheral vascular
 CC disease, myocardial ischemia, vascular intimal hyperplasia,
 CC atherosclerosis, wound healing, chronic liver disease and haemangioma
 CC formation. ZVEGF3 can also be used to modulate neurite growth and
 CC development of the nervous system, and for treating neurodegenerative
 CC diseases.
 CC
 XX Sequence 345 AA:
 XX
 XX Query Match 100.0%; Score 1848; DB 21; Length 345;
 XX Best Local Similarity 100.0%; Pred. No. 6.4e-182;
 XX Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 GRMGSGTVPGKQTSKGNHRIREFVDEYPPSEPGCIHYSIIMPOVETTSVLPSS 180
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 Db 301 VTKKHYEVLQLRPKTGKGLHKSITDVALEHHECDCCVCGNAG 345

RESULT 3

AAY84559.
 ID AAY84559 standard; Protein; 345 AA.
 XX
 AC AAY84559;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE A murine platelet-derived growth factor C (PDGF-C).
 XX
 KM Platelet-derived growth factor C; PDGF-C; cell proliferation;
 KM growth factor; heparin; connective tissue; wound healing; VEGF-F;
 KM fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
 KM chorioarcinoma; Wilms tumour; megakaryoblastic leukaemia;
 KM lung carcinoma; erythroleukemia; tissue remodelling.
 XX
 OS Mus sp.
 XX
 PN WO200018212-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 30-SEP-1999; 99WO-US22668.
 XX
 PR 30-SEP-1998; 98US-0102461.
 PR 12-NOV-1998; 98US-0108109.
 PR 03-DEC-1998; 98US-0110749.
 PR 18-DEC-1998; 98US-0113002.
 PR 21-MAY-1999; 99US-0135426.
 PR 15-JUL-1999; 99US-0144022.
 XX
 PA (LUDM-) LUDMIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD.
 XX
 PI Eriksson U, Aase K, Lee X, Ponten A, Urtela M, Altitalo K;
 PI Oestman A, Heldin C, Betsholtz C;
 XX
 DR WPI: 2000-292954/25.
 DR N-PSDB: AAA12525.
 XX
 PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
 PT differentiation, growth and motility of cells expressing the PDGF-C
 PT receptor -
 XX
 PS Claim 27; Fig 6; 135pp; English.
 XX
 CC The present sequence represents murine platelet-derived growth factor C
 CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
 CC ability to stimulate and enhance proliferation or differentiation,
 CC and/or growth or motility of cells expressing a PDGF-C receptor.

CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC chorioarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 21; Length 345;

Best local Similarity 100.0%; Pred. No. 6.4e-182;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 PKPHTYPRNMVLWVRVAVDENVRIOQLFDERFGLEDDEDDICKYDFVEEPPSDGSYL 120
 QY 121 GRMGSGTVPGKQTSKGNHRIREFVDEYPPSEPGCIHYSIIMPOVETTSVLPSS 180
 Db 121 GRMGSGTVPGKQTSKGNHRIREFVDEYPPSEPGCIHYSIIMPOVETTSVLPSS 180
 QY 181 LSLDLLNNVATFASSTLEELIRYLEPDRMOVDLSLKPMTQLGKAPLYGKSKKVVNLN 240
 Db 181 LSLDLLNNVATFASSTLEELIRYLEPDRMOVDLSLKPMTQLGKAPLYGKSKKVVNLN 240
 QY 241 LKEEVKLYSCTPRNFVSISREELKRTDTTFWPGCLVYKRGCGNACCLHNCNCCQVPRK 300
 Db 241 LKEEVKLYSCTPRNFVSISREELKRTDTTFWPGCLVYKRGCGNACCLHNCNCCQVPRK 300
 QY 301 VTKKHYEVLQLRPKTGKGLHKSITDVALEHHECDCCVCGNAG 345
 Db 301 VTKKHYEVLQLRPKTGKGLHKSITDVALEHHECDCCVCGNAG 345

RESULT 4

AAE00998 standard; Protein; 345 AA.

AAE00998;

04-JUL-2001 (first entry)

Mouse zveg3 protein.

KM Mouse; zveg3 antagonist; cell proliferation; stellate cell activation;
 KM extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KM platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KM VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KM chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KM diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KM asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KM diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
 KM pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KM bronchiolitis obliterans; organising pneumonia; transplant vasculopathy;
 KM fibroproliferative disorder.

Mus musculus.

WO200128586-A1.

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XX PD 26-APR-2001.
XX PF 23-OCT-2000: 2000MO-US29270.
XX PR 21-OCT-1999: 990US-0161653.
XX PR 12-NOV-1999: 990US-0165255.
XX PR 01-AUG-2000: 2000US-0222223.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Gilbertson DG:
XX DR WPI: 2001-300278/31.
XX DR N-PSDB: AAD04650.
XX PT use of zvegf3 antagonist for reducing fibroproliferative disorder of
XX PT kidney, liver and bone, reducing extracellular matrix production,
XX PT treating fibrosis or reducing stellate cell activation in mammal
XX PS Example 2; Fig 2; 70pp; English.
XX CC The patent discloses materials and methods for reducing cell
XX CC proliferation or extracellular matrix production, treating fibrosis and
XX CC reducing stellate cell activation in a mammal. The method comprises
XX CC administering a composition containing a zvegf3 antagonist in combination
XX CC with a delivery vehicle. The zvegf3 is a protein that is structurally
XX CC related to platelet-derived growth factor (PDGF) and the vascular
XX CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
XX CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
XX CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
XX CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
XX CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
XX CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
XX CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
XX CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
XX CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
XX CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
XX CC fibrotic disorders of pancreas, fibroproliferative disorders of the
XX CC vasculature such as transplant vasculopathy and fibroproliferative
XX CC disorders of the bone such as osteopetrosis and hyperostosis.
XX CC The present sequence is mouse zvegf3 protein.
XX SQ Sequence 345 AA:

```

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Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 6, 4e-182;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLGLLLLTALAGORTGTRAESNLSKQLQSSDKQNGVOPRHRVVTISGNSIHS 60
QY 61 PKRPHYPRMNVLMVRLVAVDENVRIDLTDERGLEDPEDDIDCKDFVEVEEPPSDG 120
DB 61 PKRPHYPRMNVLMVRLVAVDENVRIDLTDERGLEDPEDDIDCKDFVEVEEPPSDG 120
QY 121 GRMGSGTGVGKQTSKNHRIKRVSDSEYPPSPGFCIHSTIMPQVETTSVPLPSS 180
DB 121 GRMGSGTGVGKQTSKNHRIKRVSDSEYPPSPGFCIHSTIMPQVETTSVPLPSS 180
QY 181 LSLDLLNNAVTAFTSEELIRYLEPDRMAYDLDSLXKPTMQLGKAFLYGKRSKRVN 240
DB 181 LSLDLLNNAVTAFTSEELIRYLEPDRMAYDLDSLXKPTMQLGKAFLYGKRSKRVN 240
QY 241 LKEEVKILSTPRNFSVSIIEELKRTDTIPWPGCLLYKRCGGACCLAHNCNECQVPRK 300
DB 241 LKEEVKILSTPRNFSVSIIEELKRTDTIPWPGCLLYKRCGGACCLAHNCNECQVPRK 300
QY 301 VTKKHYEVLQLRPTGVKGLHKSILTDVALHHEBCDCVCNGNAGG 345
DB 301 VTKKHYEVLQLRPTGVKGLHKSILTDVALHHEBCDCVCNGNAGG 345

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RESULT 5
AAB47890
ID AAB47890 standard; Protein; 345 AA.
XX AC AAB47890:
XX DT 16-MAY-2002 (first entry)
XX DE Mouse zvegf3.
XX KW Human; mouse; zvegf3; zvegf4; platelet derived growth factor;
XX KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;
XX KW osteoblast; chondrocyte; bony defect; fracture; bone graft;
XX KW Implant; periodontal pocket; osteoclast; bone marrow stem cell;
XX KW osteoporosis.
XX OS Mus musculus.
XX PN US2002004225-A1.
XX PD 10-JAN-2002.
XX PF 29-MAR-2001: 2001US-0823033.
XX PR 07-DEC-1998: 98US-111173P.
XX PR 06-JUL-1999: 99US-142576P.
XX PR 21-OCT-1999: 99US-161653P.
XX PR 12-NOV-1999: 99US-165255P.
XX PR 31-MAR-2000: 2000US-193733P.
XX PR 07-DEC-1999: 99US-0457066.
XX PA (HART/) HART C E.
XX PA (GILB/) GILBERTSON D G.
XX PI Hart CE, Gilbertson DG:
XX DR WPI: 2002-171026/22.
XX DR N-PSDB: AAI72444.
XX PT Promoting growth of bone, ligament or cartilage in a mammal, involves
XX PT administering to the mammal a protein which comprises growth factor
XX PT domain of zvegf3 protein, a homolog of platelet-derived growth factor
XX PT
XX PS Claim 1; Page 19-20; 31pp; English.
XX CC The sequences given in AAB4789-90 represent human and mouse zvegf3,
XX CC respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog
XX CC and it was used in the method of the invention for promoting growth of
XX CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
XX CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
XX CC protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3
XX CC protein, with a delivery vehicle. The method of the invention is useful
XX CC for promoting growth of bone, ligament or cartilage in a mammal, where
XX CC the composition is administered at a site of a bony defect, preferably
XX CC a fracture, bone graft site, implant site, or periodontal pocket, and
XX CC for stimulating proliferation of osteoblasts or chondrocytes in a
XX CC mammal. It is further useful for promoting proliferation of osteoblasts,
XX CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
XX CC marrow stem cells are harvested from a patient prior to culture. The
XX CC method is therefore useful for treating osteoporosis.
XX SQ Sequence 345 AA:

```

```

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 6, 4e-182;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGLLLLTALAGORTGTRAESNLSKQLQSSDKQNGVOPRHRVVTISGNSIHS 60
DB 1 MLLGLLLLTALAGORTGTRAESNLSKQLQSSDKQNGVOPRHRVVTISGNSIHS 60

```

QY 61 PKFPHTPRNMYLVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSYL 120
 DB 61 PKFPHTPRNMYLVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSYL 120
 QY 121 GWMCGSGVPGKQTSKGNHIRIRFVSDEYFSEPGFCHYSTIMPOVETTSPSVLPSS 180
 DB 121 GWMCGSGVPGKQTSKGNHIRIRFVSDEYFSEPGFCHYSTIMPOVETTSPSVLPSS 180
 QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDLSLYKPTWOLGKAFLYGKSKYVNLNL 240
 DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDLSLYKPTWOLGKAFLYGKSKYVNLNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 QY 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
 DB 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 6

AAE13213
 ID AAE13213 standard; Protein: 345 AA.

AC AAE13213;

DT 12-FEB-2002 (first entry)

DE Mouse platelet-derived growth factor (PDGF-C) protein.

KW Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;
 cardiac hypertrophy; fibrosis.

OS Mus sp.

PN WO200172132-A1.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US09855.

PR 28-MAR-2000; 2000US-192507P.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Eriksson U, Li X, Ponten A, Aase K, Li H;

DR WPI: 2002-010700/01.

PT A transgenic animal over-expressing platelet derived growth factor C is
 useful to study and find therapy for disease associated with PDGF-C
 over-expression, including cardiac hypertrophy and fibrosis

PS Example 4: Page 42-43; 48bp; English.

CC The patent discloses a method for producing a transgenic, non-human
 CC animal over-expressing a platelet derived growth factor C (PDGF-C),
 CC or its functional fragment or analogue. The method involves introducing
 CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing
 CC the cell into a non-human animal and allowing the cell to develop into
 CC a transgenic, non-human animal. The transgenic animal is useful as a
 CC model to study disease states characterised by over-expression of PDGF-C
 CC and to find therapy for those diseases, particularly hypertrophy and
 CC fibrosis in various organs including the heart. The present sequence
 CC is PDGF-C protein from mouse.

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6,4e-182;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHHERVYITSGNGSIHS 60
 DB 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHHERVYITSGNGSIHS 60
 QY 61 PKFPHTPRNMYLVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSYL 120
 DB 61 PKFPHTPRNMYLVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSYL 120
 QY 121 GWMCGSGVPGKQTSKGNHIRIRFVSDEYFSEPGFCHYSTIMPOVETTSPSVLPSS 180
 DB 121 GWMCGSGVPGKQTSKGNHIRIRFVSDEYFSEPGFCHYSTIMPOVETTSPSVLPSS 180
 QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDLSLYKPTWOLGKAFLYGKSKYVNLNL 240
 DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDLSLYKPTWOLGKAFLYGKSKYVNLNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 QY 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
 DB 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 7

AAV33679
 ID AAV33679 standard; Protein: 345 AA.

AC AAV33679;

DT 11-JAN-2000 (first entry)

DE Human VEGF-E protein.

KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.

OS Homo sapiens.

PN WO9947677-A2.

PD 23-SEP-1999.

PF 10-MAR-1999; 99WO-US05190.

PR 17-MAR-1998; 98US-0040220.

PR 02-NOV-1998; 98US-0184216.

PA (GETH) GENENTECH INC.

PI Ferrara N, Kuo SS;

DR WPI: 1999-580306/49.

DR N-PSDB: AA223691.

PT New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy

PS Claim 1: Fig 2: 122pp; English.

CC This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tripartite, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to

PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI: 1999-551358/46.
DR N-PSDB; AA234296.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
PS Claim 12; Fig 207; 530pp; English.
XX
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23891 to
CC AA23438, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
CC
CC
SQ Sequence 345 AA:
Query Match 90.2%; Score 1667; DB 20; Length 345;
Best Local Similarity 87.0%; Pred. No. 3.2e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGORTGTRAESNLSKQLQSSDKQNGVOPRHERVYTISGNSIHS 60
DB 1 MSFLGLLLTSAAGROGTQAESNLSKQFSSNKEQNGVOPRHERITVSTNGSIHS 60
QY 61 PRPHPTPRNNVLMVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFVEEPPSDGSVYL 120
DB 61 PRPHPTPRNNVLMVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPKGKTSKGNHRIREFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPESA 180
DB 121 GRMGSGTVPKGKTSKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPESA 180
QY 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLKPWOLGKAFIYGGKSKVYNLNL 240
DB 181 LPSDLLNNAITAFSTLEDLIRYLEPDRMOVDLSLKPWOLGKAFIYGGKSKRVVDLNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACACCLNHCNCCQCVPRK 300
DB 241 LTFEVALYSCPTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACACCLNHCNCCQCVPRK 300
QY 301 VTKKHYEVLQLRPKTGKGLHNSLTDVALEHNEECDCVCRGNAG 345
DB 301 VTKKHYEVLQLRPKTGKGLHNSLTDVALEHNEECDCVCRGNAG 345
RESULT 9
AA30023

ID AA30023 standard; Protein; 345 AA.
XX
XX AA30023;
AC
XX
DT 11-OCT-1999 (first entry)
XX
XX Human vascular endothelial growth factor related protein.
DE
XX Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
XX Homo sapiens.
OS
XX MO9937671-A1.
PN
XX 29-JUL-1999.
PD
XX
XX 26-JAN-1999; 99WO-US01574.
PF
XX
XX 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0088089.
PR 24-JUN-1998; 98US-0090544.
XX
XX
PA (ELIL) LILLY & CO ELI.
XX
XX
PI Dou S, Na S, Song HY;
XX
XX WPI: 1999-458680/38.
DR N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
XX
CC The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
CC
CC
SQ Sequence 345 AA:
Query Match 90.2%; Score 1667; DB 20; Length 345;
Best Local Similarity 87.0%; Pred. No. 3.2e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGORTGTRAESNLSKQLQSSDKQNGVOPRHERVYTISGNSIHS 60
DB 1 MSFLGLLLTSAAGROGTQAESNLSKQFSSNKEQNGVOPRHERITVSTNGSIHS 60
QY 61 PRPHPTPRNNVLMVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFVEEPPSDGSVYL 120
DB 61 PRPHPTPRNNVLMVRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPKGKTSKGNHRIREFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPESA 180
DB 121 GRMGSGTVPKGKTSKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPESA 180
QY 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLKPWOLGKAFIYGGKSKVYNLNL 240
DB 181 LPSDLLNNAITAFSTLEDLIRYLEPDRMOVDLSLKPWOLGKAFIYGGKSKRVVDLNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACACCLNHCNCCQCVPRK 300
DB 241 LTFEVALYSCPTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACACCLNHCNCCQCVPRK 300

QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAG 345
 |||||||||||||||||||||||||||||||||||||||
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAG 345

RESULT 10
 AAB48657
 ID AAB48657 standard; Protein; 345 AA.
 XX

AC AAB48657;

DT 09-MAR-2001 (first entry)

XX Human zvegfg3, SEQ ID NO:33.

DE Human zvegfg3, SEQ ID NO:33.
 XX
 KW Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
 KW immunomodulation; hepatic.

OS Homo sapiens.

XX WO200066736-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000MO-US40047.

XX 03-MAY-1999; 9905-0304216.

XX 10-NOV-1999; 9905-0164463.

XX 04-FEB-2000; 2000US-0180169.

PA (ZYMO) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI: 2000-687541/67.

DR N-PSDB; AAC81582.

PT Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -

XX Claim 48; Page 125-126; 143pp; English.

XX The invention relates to the human growth factor homologue zvegfg4
 CC (AAB48653), and nucleic acids encoding it (AAC81553). zvegfg4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. zvegfg4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cystine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. zvegfg4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
 CC fusions; expression constructs and host cells comprising human zvegfg4
 CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
 CC which binds to human zvegfg4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zvegfg4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zvegfg4 gene of a patient. zvegfg4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly useful for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells

CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents human zvegfg3.
 CC XX

SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 21; Length 345;
 Best Local Similarity 87.0%; Pred. No. 3.2e-163;
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVYTSNGSIHS 60
 DB 1 MSLEGLLLLSALAGQRTGTRAESNLSSKQFSSNKQNGVQDPRHRRVYTSNGSIHS 60
 QY 61 PKPPTTYPRNMVLYWRVLAADENRIQLTPDERGLEDPPDDICKYDFVEVEPSDGL 120
 DB 61 PKPPTTYPRNTVLYWRVLAADENRIQLTPDERGLEDPPDDICKYDFVEVEPSDGL 120
 QY 121 GRWGSCTVPGKQTSKNHRIREFVSDYFPEPFCIHYSIIMPQVETTSVLPSS 180
 DB 121 GRWGSCTVPGKQTSKNHRIREFVSDYFPEPFCIHYSIIMPQVETTSVLPSS 180
 QY 181 LSDDLNNAYTAPSTLEELIRYLEPDRWYDLSLYKPTMQLGKAPLYKSKVNL 240
 DB 181 LPDNLNNAYTAPSTLEELIRYLEPDRWYDLSLYKPTMQLGKAPLYKSKVNL 240
 QY 241 LKEEVLKSCYCPNRFVSIREELKRTDTIFWPGCLLYKRCGNACCLHNCNEQCVPRK 300
 DB 241 LKEEVLKSCYCPNRFVSIREELKRTDTIFWPGCLLYKRCGNACCLHNCNEQCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAG 345
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAG 345

RESULT 11

XX AAB24250
 ID AAB24250 standard; Protein; 345 AA.

XX AAB24250;

XX 08-FEB-2001 (first entry)

XX Human platelet-derived growth factor related protein LP8.

XX Human; platelet derived growth factor related protein; LP8; VEGF;

XX vascular endothelial growth factor h; tissue regeneration; vulnery;

XX atherosclerosis; PDGF-related protein; antiarteriosclerotic.

XX Homo sapiens.

XX WO200059940-A2.

XX 12-OCT-2000.

XX 24-MAR-2000; 2000MO-US06427.

XX 06-APR-1999; 9905-0127913.

XX (ELIL) LILLY & CO ELI.

XX Hammond LJ, Na S;

XX WPI: 2000-664991/64.

XX N-PSDB; AAC64426.

PT Enhancing tissue growth and promoting wound healing by administering
 PT platelet-derived growth factor related protein, LP8 or its analog and
 PT treating atherosclerosis by administering LP8 antagonist -
 PS Claim 4; Page 63-64; 64pp; English.

XX The present invention describes a method for enhancing tissue growth.

CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated Lp8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an Lp8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth
 CC muscle growth. Antagonists of Lp8 are useful for treating
 CC atherosclerosis. The present sequence represents human Lp8, which is
 CC also called VEGFh.

XX Sequence 345 AA:

Query Match 90.2%; Score 1667; DB 21; Length 345;

Best Local Similarity 87.0%; Pred. No. 3.2e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVTTSGNSIHS 60
 DB 1 MSLLFGLLLTSLAGORGTQAESNLSSKFQSSNKEQNGVODPOHERITVTSGNSIHS 60
 QY 61 PRFPHYPRNNMVLWRLVAVDENVRQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 DB 61 PRFPHYPRNNMVLWRLVAVDENVRQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 QY 121 GRMCGSGTVPGKQTSKGNIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 DB 121 GRMCGSGTVPGKQTSKGNIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMVDLSLYKPTWOLGKAFVGRKSRVVDLNL 240
 DB 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMVDLSLYKPTWOLGKAFVGRKSRVVDLNL 240
 QY 241 LKEEVKLYSCFPRNFVSSTIREELKRTDTLFWPGCLLVKRCGGACACCLNCCQCVPRK 300
 DB 241 LKEEVKLYSCFPRNFVSSTIREELKRTDTLFWPGCLLVKRCGGACACCLNCCQCVPRK 300
 QY 301 VTKKYEVLQLRPKTGVKGLHKSLLTDVLEHHEECDCVCRGNAGG 345
 DB 301 VTKKYEVLQLRPKTGVKGLHKSLLTDVLEHHEECDCVCRGNAGG 345

RESULT 12

AAB44322 standard; Protein; 345 AA.

XX AAB44322;

DT 08-FEB-2001 (first entry)

DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.

KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 expressed sequence tag; detection; cancer.

XX Homo sapiens.

PN WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US04341.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99US-0162813.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.

XX (GENTH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fillauroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Peoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
 DR WPI: 2000-611443/58.
 DR N-PSDB: AAC78582.

PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities.

PS Claim 12; Fig 207; 636pp; English.

CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA:

Query Match 90.2%; Score 1667; DB 21; Length 345;

Best Local Similarity 87.0%; Pred. No. 3.2e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVTTSGNSIHS 60
 DB 1 MSLLFGLLLTSLAGORGTQAESNLSSKFQSSNKEQNGVODPOHERITVTSGNSIHS 60
 QY 61 PRFPHYPRNNMVLWRLVAVDENVRQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 DB 61 PRFPHYPRNNMVLWRLVAVDENVRQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 QY 121 GRMCGSGTVPGKQTSKGNIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 DB 121 GRMCGSGTVPGKQTSKGNIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMVDLSLYKPTWOLGKAFVGRKSRVVDLNL 240
 DB 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMVDLSLYKPTWOLGKAFVGRKSRVVDLNL 240
 QY 241 LKEEVKLYSCFPRNFVSSTIREELKRTDTLFWPGCLLVKRCGGACACCLNCCQCVPRK 300
 DB 241 LKEEVKLYSCFPRNFVSSTIREELKRTDTLFWPGCLLVKRCGGACACCLNCCQCVPRK 300
 QY 301 VTKKYEVLQLRPKTGVKGLHKSLLTDVLEHHEECDCVCRGNAGG 345
 DB 301 VTKKYEVLQLRPKTGVKGLHKSLLTDVLEHHEECDCVCRGNAGG 345

RESULT 13

AAB10633 standard; Protein; 345 AA.

XX AAB10633;

```

XX 19-JAN-2001 (first entry)
DT Human RACE generated VEGF-X protein.
XX
DE
XX VEGF-X; vascular endothelial growth factor; human; vulnerrary; cyrostatic;
KM antithemmatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KM angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KM rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KM tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KM venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99MO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Goslowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAAI1951.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX disclosure; Fig 6; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerrary, cyrostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention.
XX
XX Sequence 345 AA:
SQ
Query Match 90.2%; Score 1667; DB 21; Length 345;
Best Local Similarity 87.0%; Pred. No. 3, 2e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
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DB 1 MSFGLLLTLAGORGTQAESNLSKFOFSNKEQNGVQDPHRRITVTISGSIHS 60
OY 61 PKPRHTPRMMVLWVRVVAADENVRITQTFDERGLEDPEDDICKYFVEVEEESDSVL 120
DB 61 PREPHYPRMTVLWVRVVAEENWQITQTFDERGLEDPEDDICKYFVEVEEESDSTIL 120
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DB 121 GRMGSGTVGKQTSKGNHRIKRFVSDPEPSPGFCIHHSIIMPQVTEFTSPSVLPSS 180

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OY 181 LSIDLNNNAVAFSTLEELIRYLEPDRMOYDLSELYKPTMOLLGKAFLYGRKSKVNLNL 240
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DB 241 LTEEVRILYSTPRMFSVSIIEELKRTDTTFWPGCLLYKRCGGNACCLAHNCNCCQCPRK 300
OY 301 VTKKYHEVLQRPKTGVKGLHKSILTVALHEHRECDVCGRGNAGG 345
DB 301 VTKKYHEVLQRPKTGVKGLHKSILTVALHEHRECDVCGRGNAGG 345
RESULT 14
AABI0635
ID AABI0635 standard; Protein; 345 AA.
XX
XX AABI0635;
XX
XX 19-JAN-2001 (first entry)
XX
XX Human VEGF-X protein #1 isolated from clones 4 and 7.
XX
XX VEGF-X; vascular endothelial growth factor; human; vulnerrary; cyrostatic;
KM antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KM angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KM rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KM tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KM venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99MO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Goslowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAAI1955.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX disclosure; Fig 9; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerrary, cyrostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
XX

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SQ Sequence 345 AA: 90.2% Score 1667; DB 21: Length 345; Query Match Best Local Similarity 87.0%; Pred. No. 3,2e-163; Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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 1 MSLEFGLLLTSLAGORGTQAESNLSSKRFQSSNKEONGVOPRHRITVTNSIHS 60
 Db 61 PRPHPTYPNNMVLWRLVAVDENVRIOQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
 1 PRPHPTYPNNMVLWRLVAVDENVRIOQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
 Db 61 PRPHPTYPNNMVLWRLVAVDENVRIOQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
 QY 121 GRMGSGTVPKGKQISGNQIRIRFVDEYFSPSGFCIHNIYMPQFTEAVSPSVLPSSA 180
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RESULT 15
 AAB10644
 ID AAB10644 standard; Protein: 345 AA.

AC AAB10644;
 XX 19-JAN-2001 (first entry)
 XX Human VEGF-X protein #4.
 DE Human VEGF-X protein #4.
 KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytoskeletal;
 KW anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.
 KM
 XX Homo sapiens.
 OS
 XX
 PN WO200037641-A2.
 XX 29-JUN-2000.
 PD
 XX 21-DEC-1999; 99WO-US30503.
 PF
 XX 22-DEC-1998; 98GB-0028377.
 PR 18-MAR-1999; 99US-0124967.
 PR 08-NOV-1999; 99US-0164131.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Gordon RD, Sprengel JJ, von JR, Dijkmans JH, Goslowska A;
 PI Dhanraj SN, Xu J;
 XX WPI: 2000-442669/38.
 DR N-PSDB; AAA71990.
 XX
 PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
 XX
 PS Disclosure; Fig 30B; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnery, cytoskeletal, anti-rheumatic, antiarthritic, antipsoriatic and
 CC anti-diabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents a human VEGF-X protein
 CC described in the method of the invention.
 XX

SQ Sequence 345 AA: 90.2% Score 1667; DB 21: Length 345; Query Match Best Local Similarity 87.0%; Pred. No. 3,2e-163; Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGRTAESNLSSKRLQSSDKONGVOPRHRVYTISGNSIHS 60
 1 MSLEFGLLLTSLAGORGTQAESNLSSKRFQSSNKEONGVOPRHRITVTNSIHS 60
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 QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
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 Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
 QY 301 VTKKHYEVLQLRKKTGVKGLHKS/LTDVLEHHECDCCVCRGSGTG 345
 301 VTKKHYEVLQLRKKTGVKGLHKS/LTDVLEHHECDCCVCRGSGTG 345
 Db 301 VTKKHYEVLQLRKKTGVKGLHKS/LTDVLEHHECDCCVCRGSGTG 345

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 Job time : 34.5 secs

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GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 09:08:16 ; Search time 26.5 Seconds
(without alignments)
1043.199 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLTSLAGQRTGT.....DVALEHHECDCCVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1848	100.0	345	US-09-852-209A-7	Sequence 7, Appl1
2	1848	100.0	345	US-10-139-583-43	Sequence 43, Appl1
3	1848	100.0	345	US-09-823-033-4	Sequence 4, Appl1
4	1848	100.0	345	US-09-818-943-2	Sequence 2, Appl1
5	1667	90.2	345	US-09-978-295A-488	Sequence 488, App
6	1667	90.2	345	US-09-978-697-488	Sequence 488, App
7	1667	90.2	345	US-09-978-192A-488	Sequence 488, App
8	1667	90.2	345	US-10-139-583-2	Sequence 488, App
9	1667	90.2	345	US-09-999-832A-488	Sequence 488, App
10	1667	90.2	345	US-09-978-189-488	Sequence 488, App
11	1667	90.2	345	US-10-028-072-286	Sequence 286, App
12	1667	90.2	345	US-10-121-049-286	Sequence 286, App
13	1667	90.2	345	US-10-123-904-286	Sequence 286, App
14	1667	90.2	345	US-10-140-470-286	Sequence 286, App
15	1667	90.2	345	US-09-796-753-6	Sequence 6, Appl1
16	1667	90.2	345	US-10-175-746-286	Sequence 286, App
17	1667	90.2	345	US-10-176-918-286	Sequence 286, App
18	1667	90.2	345	US-10-176-921-286	Sequence 286, App
19	1667	90.2	345	US-10-103-197-4	Sequence 4, Appl1

20	1667	90.2	345	US-10-137-865-286	Sequence 286, App
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43	1667	90.2	345	US-10-013-921A-488	Sequence 488, App
44	1667	90.2	345	US-10-123-108-286	Sequence 286, App
45	1667	90.2	345	US-10-123-236-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-852-209A-7
Sequence 7, Application US/09852209A
Patent No. US20020164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PORTEN, Annica
APPLICANT: UTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al 1-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-852-209A-7
Query Match 100.0% Score 1848: DB 9: Length 345:
Best Local Similarity 100.0% Pred. NO. 1.5e-155:
Matches 345: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 MLLGLLLTSLAGQRTGTASNLSSKQLQSLSDKEQGVQDPFRHRRVVTISGNCSHS 60

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Db      61 PKPHTYPRMVMVWVRVAVDENVRIOLTFDERFGLDEPDIDCKYFVVEEPPSDGSVL 120
QY      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVETTSFVLPSS 180
Db      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVETTSFVLPSS 180
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RESULT 2

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US-10-139-583-43
; Sequence 43, Application US/10139583
; Patent No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRK
; ORGANISM: Mus musculus
US-10-139-583-43

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Query Match 100.0%; Score 1848; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.5e-155;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRK
; ORGANISM: Mus musculus
US-09-823-033-4

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Query Match 100.0%; Score 1848; DB 10; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.5e-155;

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QY      181 LSLDLLNNAVTAFTLEELIRYLEPDRMOWDLSLYKPTMQLGKAFLYGKSKSVNVLN 240
Db      181 LSLDLLNNAVTAFTLEELIRYLEPDRMOWDLSLYKPTMQLGKAFLYGKSKSVNVLN 240
QY      241 LKEEVKLYSCTPRNFSYSIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
Db      241 LKEEVKLYSCTPRNFSYSIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQCVPRK 300
QY      301 VTKKYEVLQLRPKTVGKGLHKSITDVALEHHECDVCVCGNAG 345
Db      301 VTKKYEVLQLRPKTVGKGLHKSITDVALEHHECDVCVCGNAG 345

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RESULT 4

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US-09-818-943-2
; Sequence 2, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: Li, Xuli
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: Li, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWT
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7

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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: prt
ORGANISM: Murinae gen. sp.
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 1-5e-155;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHRYVTTSGNSIHS 60
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QY 61 PKPHTYPRNMVLYRVAVDENVRQLTFDERFGLEDEDDICKYDFEVEEPSGSVL 120
DB 61 PKPHTYPRNMVLYRVAVDENVRQLTFDERFGLEDEDDICKYDFEVEEPSGSVL 120
QY 121 GRMCGSTVPGKOTSKGNHIRIFVSDSEYFSPGFCIHYSITMPQVETTSPSVLPPSS 180
DB 121 GRMCGSTVPGKOTSKGNHIRIFVSDSEYFSPGFCIHYSITMPQVETTSPSVLPPSS 180
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMOVDLSLYKPTWQLGKAFLYKSKSVVNL 240
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMOVDLSLYKPTWQLGKAFLYKSKSVVNL 240
QY 241 LKEEVKLVSTPRNFSVSIRELKRDTTFWPGCLLYKRCGNGACCLNCECCVPRK 300
DB 241 LKEEVKLVSTPRNFSVSIRELKRDTTFWPGCLLYKRCGNGACCLNCECCVPRK 300
QY 301 VKKXHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRNAGG 345
DB 301 VKKXHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRNAGG 345

RESULT 5
US-09-978-295A-488
Sequence 488, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desmoyers, Luc
APPLICANT: Eaton Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1 6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTGTGAESNLSSKLLQSSDKQNGVQDPHRRVYTISGNSIHS 60
1 MSFGLLLTSLALAGTGTGAESNLSSKLLQSSDKQNGVQDPHRRVYTISGNSIHS 60
Db 1 MLLGLLLTSLALAGTGTGAESNLSSKLLQSSDKQNGVQDPHRRVYTISGNSIHS 60
QY 61 PKRPHYTPRMVLYWRLVANDENVRIQITDERFGLEDPEDDICKIDFVVEEPSDGSVL 120
61 PKRPHYTPRMVLYWRLVANDENVRIQITDERFGLEDPEDDICKIDFVVEEPSDGSVL 120
Db 61 PKRPHYTPRMVLYWRLVANDENVRIQITDERFGLEDPEDDICKIDFVVEEPSDGSVL 120
QY 121 GRMGSGTVPKQTSKGNHRIREFVSPDEPSPGFCIHSIMPOVTEITSSVLPSS 180
121 GRMGSGTVPKQTSKGNHRIREFVSPDEPSPGFCIHSIMPOVTEITSSVLPSS 180
Db 121 GRMGSGTVPKQTSKGNHRIREFVSPDEPSPGFCIHSIMPOVTEITSSVLPSS 180
QY 181 LSLDLLNNAVTASLEELIRYLEPDRQYDLSLXKPTWOLLGKAFLYGRKSKVYNLNL 240
181 LSLDLLNNAVTASLEELIRYLEPDRQYDLSLXKPTWOLLGKAFLYGRKSKVYNLNL 240
Db 181 LSLDLLNNAVTASLEELIRYLEPDRQYDLSLXKPTWOLLGKAFLYGRKSKVYNLNL 240
QY 241 LKEEVKLYSTPRNFVSSTIEELKRTDTITWPGCLLVKRCGCMACCLHNCNCQCVPRK 300
241 LKEEVKLYSTPRNFVSSTIEELKRTDTITWPGCLLVKRCGCMACCLHNCNCQCVPRK 300
Db 241 LKEEVKLYSTPRNFVSSTIEELKRTDTITWPGCLLVKRCGCMACCLHNCNCQCVPRK 300
QY 301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHNEECDCVCGRNAGG 345
301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHNEECDCVCGRNAGG 345
Db 301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHNEECDCVCGRNAGG 345

RESULT 6
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjaavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 90.2%; Score 1667; DB 9; Length 345;
Best local Similarity 87.0%; Pred. No. 1.6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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Db 61 PRPHYPRMVLVWRLVAVDENVRIOITFDERGLEDPEDDICKIDFVEVEPSDGSVL 120
QY 121 GRMGSGTVGKOTSKGNHRIKRVSDYPPSPFCIHYSIIMPQVTEHTSPSVLPSS 180
Db 121 GRMGSGTVGKOTSKGNHRIKRVSDYPPSPFCIHYSIIMPQVTEHTSPSVLPSS 180
QY 181 LSIDLNNAVTAFTLEELIRYLEPPRMOYDLDSLYKPTWQLLGAFLYKRSKVVNL 240
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QY 241 LKEEVKISTPKNFSVSTIEELKRTDTTWPQGLVYKRGGNCACCLHNCNECCVP 300
Db 241 LKEEVKISTPKNFSVSTIEELKRTDTTWPQGLVYKRGGNCACCLHNCNECCVP 300
QY 301 VTKKYEVLQLRKPTGYKGLKSLTDVALHEHBCDCVCGNAGG 345
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RESULT 7

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US-09-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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89 PRIOR APPLICATION NUMBER: 60/085697
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[illegible]

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RESULT 8
US-10-139-583-2
; Sequence 2, Application US/10139583
; Patent No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-2

Query Match          90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1,6e-119;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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Db 1 MSLEGLLLTSLAGQRTGTAEENSSKLOLSDKEONGQODRHRHVVTISGNGSIHS 60
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Db 61 PRPHPTPRMTVLVWRLVADEVNRIQLTFDERGLEDDPEDDICKYDFVEVEEPPSDSVL 120
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QY 121 GRWGSGTIVGKQTSKGNHRIKRVSDIYPPSEFGCIHNSIIMPQVTEITTSBVLPPSS 180
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QY 241 LKEEVKLYSCTPRNFSVSIREEIKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPRK 300
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QY 301 VTKKYEVLQLRPTGYKGLKSLTDVALKHEHCCDCVCSNAGG 345
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RESULT 9
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Hong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavyn, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-03-31
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Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
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Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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DB 181 LPDILLNNITAFSTLEELIRYIEPRMOVDLSLKPTWOLGKAFLYGKKRSVVDLNL 240
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QY 241 LKEEVLKYSTPKNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
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DB 241 LKEEVLKYSTPKNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 VTKKHEVLQLRPKTVGKGLKSLTDVALEHHECCDVCGRNAG 345
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 VTKKHEVLQLRPKTVGKGLKSLTDVALEHHECCDVCGRNAG 345
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-028-072-286
? Sequence 286, Application US/10028072
? Publication No. US2003000431A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: Deforge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang
? TITLE OF INVENTION:
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/10/028,072
? CURRENT FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059836
? PRIOR FILING DATE: 1997-09-24
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/062285
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/062814
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/062816
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/063045
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/063082
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/063127

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QY 301 VTKKHYEVLDLRPKTVGKGLHKSLLDVALHEHNECCDVCRCGNAG 345
Db 301 VTKKHYEVLDLRPKTVGKGLHKSLLDVALHEHNECCDVCRCNSTG 345

RESULT 14

US-10-140-470-286
; Sequence 286, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-286

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVOPRHRVYISGNGSIHS 60
Db 1 MSLFGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVOPRHRVYISGNGSIHS 60
QY 61 PKPRHTPRKMWLVWRYAVDENRVLQTLTDERFGLDEPDDEDDICKYDFVEVEEPPSDGVL 120
Db 61 PREPHTPRNTVWRLVVAEENWVLIQTLTDERFGLDEPDDEDDICKYDFVEVEEPPSDGVL 120
QY 121 GRMGSGTVGKQTSKGNHRIKRVSDSEYPPSPGFCIHYSIIMQVTEITTSPTVLPPSS 180
Db 121 GRMGSGTVGKQTSKGNHRIKRVSDSEYPPSPGFCIHYSIIMQVTEITTSPTVLPPSS 180
QY 181 LSLDLNNAATSTLEELIRYLEPDRQVDSLKPTWQLLGAFLYKKSRYVMNL 240
Db 181 LPLDLNNAATSTLEELIRYLEPDRQVDSLKPTWQLLGAFLYKKSRYVMNL 240
QY 241 LKEEVKLYSTPRNFVSISIEELKRDTITWPGCLLVKRCGGACCLHNCNECQVPRK 300
Db 241 LKEEVRLYSTPRNFVSISIEELKRDTITWPGCLLVKRCGGACCLHNCNECQVPSK 300
QY 301 VTKKHYEVLDLRPKTVGKGLHKSLLDVALHEHNECCDVCRCGNAG 345
Db 301 VTKKHYEVLDLRPKTVGKGLHKSLLDVALHEHNECCDVCRCNSTG 345

RESULT 15
US-09-796-753-6
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1

; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-6

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVOPRHRVYISGNGSIHS 60
Db 1 MSLFGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVOPRHRVYISGNGSIHS 60

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:03:41 ; Search time 55 Seconds
(without alignments)
1292.477 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLLGLLLTSLALGQRTGT.....DVALHHEHCDCVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	11	090Y71 mus musculus
2	1819	98.4	345	11	090Y71 mus musculus
3	1801	97.5	345	11	090Y71 mus musculus
4	1667	90.2	345	11	090Y71 mus musculus
5	1652	84.0	345	13	090Y71 mus musculus
6	1552	84.0	345	13	090Y71 mus musculus
7	754	40.8	370	11	090Y71 mus musculus
8	752	40.7	370	11	090Y71 mus musculus
9	750.5	40.6	364	4	090Y71 mus musculus
10	746.5	40.4	370	11	090Y71 mus musculus
11	660	35.7	290	11	090Y71 mus musculus
12	201	10.9	923	13	080Y71 mus musculus
13	192.5	10.4	691	13	057658 mus musculus
14	192	10.4	34	11	090Y71 mus musculus
15	191	10.3	977	13	091925 xenopus lae
16	186	10.1	735	13	057381 xenopus lae

17	185	10.0	926	4	090Y71 mus musculus
18	183	10.0	1015	4	090Y71 mus musculus
19	183	9.9	1012	11	090Y71 mus musculus
20	181	9.8	241	11	090Y71 mus musculus
21	176	9.5	609	4	090Y71 mus musculus
22	176	9.5	644	4	090Y71 mus musculus
23	176	9.5	704	4	090Y71 mus musculus
24	174.5	9.4	3623	4	060494 mus musculus
25	169	9.1	1008	13	090Y71 mus musculus
26	168	9.1	921	11	090Y71 mus musculus
27	165	8.9	1013	11	062381 mus musculus
28	165	8.8	1019	13	057382 mus musculus
29	162	8.8	1013	4	043897 mus musculus
30	162	8.8	1013	4	090Y71 mus musculus
31	161.5	8.7	919	13	090Y71 mus musculus
32	161.5	8.7	936	13	080Y71 mus musculus
33	160	8.7	3623	11	070244 mus musculus
34	158.5	8.6	926	11	0802Y7 mus musculus
35	158	8.5	3620	6	090Y71 mus musculus
36	157	8.5	276	4	090Y71 mus musculus
37	157	8.5	415	4	090Y71 mus musculus
38	155.5	8.4	555	4	090Y71 mus musculus
39	155.5	8.4	901	4	090Y71 mus musculus
40	155.5	8.4	901	4	090Y71 mus musculus
41	155.5	8.4	906	4	090Y71 mus musculus
42	155.5	8.4	906	4	090Y71 mus musculus
43	150.5	8.1	686	13	090Y71 mus musculus
44	149	8.1	212	11	090Y71 mus musculus
45	149	8.1	701	11	090Y71 mus musculus

ALIGNMENTS

RESULT 1
ID 090Y71 PRELIMINARY: PRT; 345 AA.
AC 090Y71;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Fallottein (platelet-derived growth factor C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RP TISSUE=OVARY;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallottein from mouse ovary."
RN Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha receptor."
CC Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF117608; AAF22516.1; -;
DR EMBL: AF266467; AAK58566.1; -;
DR MCD; MGI:1859631; Pd9fc.
DR InterPro: IPR000859; CUB_domain.
DR Pfam: PF00431; CUB_1.
DR Pfam: PF00341; PDGFC_1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGFC_1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGFC_2; 1.

SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
 Query Match 100.0%; Score 1848; DB 11; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-162;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 QY 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
 DB 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
 QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 QY 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
 DB 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
 QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
 DB 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
 QY 301 VTKKYHEVLQLRPKTYGKGLHKSITDVALEHHECDVCVCRGNAG 345
 DB 301 VTKKYHEVLQLRPKTYGKGLHKSITDVALEHHECDVCVCRGNAG 345

RESULT 2
 ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
 AC Q9JHV8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Platelet-derived growth factor C.
 GN PDGFC.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS-WEBSER/NIH;
 RX MEDLINE=20417814; PubMed=10960785;
 RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
 RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
 RT organogenesis.";
 RL Mech. Dev. 96:209-213(2000).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AF286725; AAF91483.1; -;
 DR MGD: MG1:1859631; PdGfc.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 345 AA; 38886 MW; FA1486BEDD362F8 CRC64;

Query Match 98.4%; Score 1819; DB 11; Length 345;
 Best Local Similarity 98.8%; Pred. No. 6.9e-160;
 Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 QY 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120

DB 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
 QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 QY 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
 DB 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
 QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
 DB 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
 QY 301 VTKKYHEVLQLRPKTYGKGLHKSITDVALEHHECDVCVCRGNAG 345
 DB 301 VTKKYHEVLQLRPKTYGKGLHKSITDVALEHHECDVCVCRGNAG 345

RESULT 3
 ID Q9EOX6 PRELIMINARY; PRT; 345 AA.
 AC Q9EOX6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Spinal cord-derived growth factor.
 GN RSCDGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=KIDNEY;
 RX MEDLINE=21092670; PubMed=11162582;
 RA Hamada T., Ui-Tel K., Miyata Y.;
 RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 RT SCDF/PDGF-C/fallopain.";
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB033830; BAB19969.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00341; PDGF; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;
 Best Local Similarity 96.8%; Pred. No. 3.2e-158;
 Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKDONGVODPRHRVYVITISNGSIHS 60
 QY 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
 DB 61 PKPHTYPRNMVLYWRLVAADENVRIOQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
 QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETETSPSVLPSS 180
 QY 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
 DB 181 LSLDLNNAVTAFTSEBELIRYLEPDRMOYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240

Qy	241	LKEEYKATSCPPRNFSVISIRELKRTPDIIPFGCLYKRRGGNACCLHNCNECCYPRK	300
Db	241	LKEEYKATSCPPRNFSVISIRELKRTPDIIPFGCLYKRRGGNACCLHNCNECCYPRK	300
Qy	301	VTKKTYHEVQLRPRTGVKGLKSLTDVALEHNEECDCVCROMAGC	345
Db	301	VTKKTYHEVQLRPRTGVKGLKSLTDVALEHNEECDCVCROMAGC	345

RESULT 4

ID	PRELIMINARY;	PRT;	345 AA.
Q9UL22; Q9UL23;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE Secretory growth factor-like protein FALLOTIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).			

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Tsai Y.J., Lee R.R.K., Lin S.P.,
RT "Pallotelin, a novel growth factor like gene identified in human
RL uterus.", (SEP-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE-20317014; PubMed-10858496;
RA Hamada T., UI-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGFVEGF family.";
FEBS Lett. 475:97-102(2000).

RP SEQUENCE FROM N.A.
RX MEDLINE-21347863; PubMed-11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
Riordan J.P., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
Hochstadt A.L., Humes J.M., Palmer T.E., Hart C.E.).
RA "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor.";
CC J. Biol. Chem. 276:27406-27414(2001).
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

```
DR      EMBL; AF091434; AAF00049.1; -
DR      EMBL; AB030831; BAB03266.1; -
DR      EMBL; AF260738; AAK51637.1; -
DR      InterPro; IPR000659; CUB_domn
DR      InterPro; IPR00072; CUB_domn_factor.
DR      Pfam; PF00431; CUB; 1.
DR      Pfam; PF00341; PDGF; 1.
DR      SMART; SMO0042; CUB; 1.
DR      SMART; SMO0141; PDGF; 1.
DR      PROSITE; PS01180; CUB; 1.
DR      PROSITE; PS50278; PDGF; 2, 1.
SQ      SEQUENCE 345 AA; 39029 MW;  CDE9E51F40633E78 CRC64
```

Query Match	90.28	Score 1667	DB 4	Length 345
Best Local Similarity	87.08	Pred. No. 7.8e-146		
Matches 300; Conservative	27	Mismatches 18	Indels 0	Gaps 0

QY 1 MLLGLLLLTALAGQRTGTAAESNLSSKLLSSDKQNGVQDPRHRRVVTISGNGSIHS 600

61 DEEDUEVDDNAGI UEDD UAUDEDUTOT EEDNEDOT EDEEDDIDUEDEUENNEDEDEDEDE 13

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Db      61 PRPHPTPRNTVLVWRVAEENWMIQLTDFDERFGIEDPEDICKYDFVEVEEPSGITL 120
```

QY	121	GRMGSGVPEKQKSKNGHRIPIRVSDSEYPRSPGFCIHYSIMPMQYETTSSEVLPSS	180
QY	121	GRMGSGVPEKQKSKNGHRIPIRVSDSEYPRSPGFCIHYSIMPMQYETTSSEVLPSS	180
DB	121	GRMGSGVPEKQKSKNGHRIPIRVSDSEYPRSPGFCIHYSIMPMQYETTSSEVLPSS	180
QY	181	LSDDLNNATVAFSTLEELRIYLEDPRQVQDLDSLYKPTMQLLGKAFVLYGKSKSVNML	240
DB	181	LSDDLNNATVAFSTLEELRIYLEDPRQVQDLDSLYKPTMQLLGKAFVLYGKSKSVNML	240

1

Qy	301	VTKKYHEVLQRPKTVGKGLHKS	SLTDVALENHNEECDCV	GRGNMG	345
Db	301	VTKKYHEVLQRPKTVGKGLHKS	SLTDVALENHNEECDCV	GRGNMG	345

RESULT 5

ID	GENRAT:	PRELIMINARY:	PRT:	345 AA.
AC	09NRAL:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Platelet-derived growth factor C.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NC	NCBI_TaxID=9606;			
XX				

RC TISSUE-LUNG.: PubMed=10806482; .
RX MEDLINE=20268201; PubMed=10806482; .
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Baskholm C., Heidén C.-H., Alltalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
receptor.";

```

42  NAL. CELL BIOL. 2:3025-3031(2000).
CC  1.  SIMILARITY: CONTAINS 1 CUB DOMAIN
DR  EMBL; AF244813; AAF80597.1; -.
DR  InterPro: IP0000859; CUB domain.
DR  InterPro: IP0000072; PD_growth_factor
DR  Pfam; PF00443; CUB; 1.
DR  Pfam; PF00341; PDGF; 1.
DR  SMART; SM00042; CUB; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PSS01180; CUB; 1.
DR  PROSITE; PSS0278; PDGF_2; 1.
50  SEQUENCE 345 AA; 35043 MW; 5908896

```

Query Match	90.0%	Score 1664	DB 4	Length 345
Best Local Similarity	86.7%	Pred. No. 1.5e+145		
Matches 299	Conservative 28	Mismatches 18	Indels 0	Gaps 0

```
QY      1 MLLGLLLLTALAGQRRTGTRAESNLSSKLQLSDKREQNGVDPRHERVYTISGNSIHS   60  
        | | :|::||| ||||| | :|:||||| |::|::| | |||||  
Db      1 MSLEGLLVTSALAGQRGTQAEENLSSKKQFSSNKEONGVDPOHERITVTSTGNSIHS   60
```

61 PKPHTYPRNNVLVAVDENVRIGLTFFDERGLEDDEDDICKYDFVEYEESPDSGVL 120

```
09      GRMCGSGTVEKOTSKGNHRIIRFVSDEYFPSEBFCIHYSIIMBPQVETFSPSVLPPSS 1800
```

Db 121 GRMGSGTGVKQISKGNQIRIRFVSDDEYFPSEGGCIHININVMQFTTEANVSPSYLPSPA 1800

Qy 181 LSLDLLNNAVTAFTLEELIRLEPDRMQVDLDSLYKPTWQLGKAFLYGKRSKVVNL 2400

Qy	Db
241 LKEEYKLYSCTPRNFSVSIREDEIKRTDTIFWPGCLVYKRCGGNACCLHANGNECQVPRK 3000	181 LPDDLNNATAFSTEDLIRLEPERNQDLEDELYRPTNQLGKRAVFGRKSRVYDNL 2400

Db 241 LEEVRLVSCPTPRNSVSIRBELKRTDITLFWPGCLLVKRCGGNCACCHLNCECCVPBK 300

Oy 301 VTKKHVEVLQLRPKTGVKGILKSITLDVALEHHEECDCVCRNAGG 345
|||||
|||

Db 301 VTKKHVEVLQLRPKTGVKGILKSITLDVALEHHEECDCVCNSTGG 345

RESULT 6

OY1946 PRELIMINARY: PRT: 345 AA.

AC 091946;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Spinal cord-derived growth factor.
GN SCDGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGRON; TISSUE-SPINAL CORD;
RX MEDLINE=20317014; PubMed=10856496;
RA Hamada T., U-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1;
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SMO0042; CUB; 1.
DR SMART; SMO0141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SO SEQUENCE 345 AA; 38940 MM; 97ACEA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;
Best Local Similarity 80.3%; Pred. No. 3,4e-135;
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

OY 1 MLILGLLLTSALAQRGRTGRAESNLSSKTLQSDSREONGVDPFRHERVTISNGSIHS 60
Db 1 MLILGLLLTSALAGRHRGAASDLSSKFSPPAKKEONGVDPPQHEKITITSNGSIHS 60
OY 61 PRFPHTYRRNMYLVRLVAVDENVNIQLTFEDRFGLEDPEDDICXIDYVEVEEPSDGSL 120
Db 61 PRFPHTYRRNTLVRLVAVDENVNIQLTFEDRFGLEDPEDDICXIDYVEVEEPSDGSL 120
OY 121 GWCMSGWYPGKOTSGKNHRIREFUSDEXEPSEPFCHYSITIMPOVETTPSVLPSPSS 180
Db 121 GRWCSSSVSPSQISKGMQIRIFVESDEXEPSPFCIHLYTLVVHHTEAPSSLPSPA 180
OY 181 LSIDLNNAVAFSTIELIRYLEPDRNOVDLSLYKPTWQLLAGRAFTLGKRSKYVNLT 240
Db 181 LPDLVNNNAVGSFIVEELIRYLEPDRNOVDLEDLYRPTWQLLAGRAYIGHRSRYVDNL 240
OY 241 LKEEVKLIVSCPTPRNSVSIRBELKRTDITLFWPGCLLVKRCGGNCACCHLNCECCVPBK 300
Db 241 LKEEVRLVSCPTPRNSVSIRBELKRTDITLFWPLCLLVKRCGGNCACCHLNCECCIPRK 300
OY 301 VTKKHVEVLQLRPKTGVKGILKSITLDVALEHHEECDCVCRNAGG 345
Db 301 VTKKHVEVLQLRPKTGVKGILKSITLDVALEHHEECDCVCNSTGG 345

RESULT 7

OY9BOT1 PRELIMINARY: PRT: 370 AA.

ID O9EOT1

Query Match	Best Local Similarity	40.8%	Score 754;	DB 11;	Length 370;
Matches 151;	Conservative	62;	Mismatches 86;	Indels 28;	Gaps 10;
09E9CT1:	01-MAR-2001 (TREMBLrel. 16, Created)				
AC	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Spinal_cord derived growth factor-B.				
GN	RSCDF-B.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21092670; PubMed=11162582;				
RA	Hamada T., Yi-Tel K., Imaki J., Miyata Y.;				
RT	"Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to				
RT	SCDF/PDGF-C/fallotin."				
RL	Biochem. Biophys. Res. Commun. 280:733-737(2001).				
CC	-I- SIMILARITY: CONTAINS 1 CUB DOMAIN.				
DR	EMBL, AB052170: BAB18920.1; -				
DR	InterPro: IPR000859; CUB_domain.				
DR	InterPro: IPR000072; PD_growth_factor.				
DR	Pfam: PF00431; CUB; 1.				
DR	SMART: SM00042; CUB; 1.				
DR	SMART: SM00141; PDGF; 1.				
DR	PROSITE: PS01180; CUB; 1.				
DR	PROSITE: PS50278; PDGF_2; 1.				
SQ	SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;				
Query Match	Best Local Similarity	40.8%	Score 754;	DB 11;	Length 370;
Matches 151;	Conservative	62;	Mismatches 86;	Indels 28;	Gaps 10;
0Y	37 EONGYQD-PRHEVVITSGNSIHSPKPHYPRNMVLYMRLVAVDENVRITQLTFDERFG 95				
DB	42 ESNHLDLRLROENIRVGTGHSQPRPNRYRLTLTWRLHS-QEKTRITQLAFDHOFG 100				
0Y	96 LEDPDDICKIDFVVEEPPDSG-VLGRWCGSGTVEPKOTSKGNHRIKRVSDYEPSE 153				
DB	101 LEEANDNLCRDYFVEVEYSESSITVVRNRMGHKEIPRITSRTNQIKITFPOSDYFAK 160				
0Y	154 PGFCYHSIT--MQ-----VTEET-----TSPSYLPPSLSLDLNNAVAFST 195				
DB	161 PEFKITYSFVEDFOPEANSEINSESVTSSFGSVYSHSSVM-DSTLTADALDKAIAEFT 219				
0Y	196 LEEILRYLEPPRMQYDLDLSLYKPTWQLGKAFLYGKRSKVVNLNLKEEVLVYSCPRNF 255				
DB	220 VEDLTKYFNPSAQDLENLVMDTPRYGRASY-HEKRSK-VDLRLDNDVARYSCTPRNH 277				
0Y	256 SVSTIEELKRDITVTPGCLLYKRGCGACCLAHNCNCQCPVKRYKTYEVLQLR-- 313				
DB	278 SYNLDEELKLTNAVFEPFPCLLVYRGGNGCGGLNMKSCCTSSGKTYKHYEVLKEFPGH 337				
0Y	314 -KTGVKGLHKSITDVALEHNEHCDCVC 339				
DB	338 FKRRGKAKMALVLDIQLDHEKRCDCIC 364				
RESULT 8					
09GZPO					
ID	09GZPO	PRELIMINARY:	PRT:	370 AA.	
AC	09GZPO:				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	SPINAL COND-derived growth factor-B (MSP036) (IRS-expressed growth				
DE	factor long form) (platelet-derived growth factor D).				
GN	HSCDGF-B OR IEGF OR PDGFD.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

RA Hamada T., Ue-Tai K., Imaki J., Miyata Y.;
 RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 SCDF/PDGF-C/fallotelin";
 RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=AORTA;
 RA Liu B., Liu Y.-Q., Wang X.-Y., Zhao B., Sheng H., Zhao X.-W., Liu S.,
 Xu Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
 Cao H.-Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.-Q.,
 Yuan J.G., Liew C.-C., Zhao M.S., Hui R.T.;
 RN Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=IRIS;
 RA Wistow G.;
 RT "Iris-expressed Growth Factor (IEGF).";
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX PubMed-11331881;
 RA Bergsten E., Dutela M., Li X., Pietras K., Ostman A., Heidin C.H.,
 Allitalo K., Eriksson U.;
 RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
 receptor";
 RL Nat. Cell Biol. 3:512-516(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2123180; PubMed-11331882;
 RA LaRochele W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
 Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
 RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
 RT "PDGF D, A Novel Protease-Activated Growth Factor";
 RL Nat. Cell Biol. 3:517-521(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB03832; BAB18903.1; -;
 DR EMBL: AF113216; AAG39287.1; -;
 DR EMBL: AY027517; AAK20081.1; -;
 DR EMBL: AF336376; AAK56136.1; -;
 DR EMBL: AF335584; AAK38840.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR InterPro: IPR000531; TonB_boxc.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 DR SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
 SQ

Query Match 40.7%; Score 752; DB 4; Length 370;
 Best Local Similarity 45.3%; Pred. No. 3.7e-61;
 Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

QY 37 EONGVOD-PRHRYVITISNGSIHSPKPPHYPRNMVLYRLVAVDENRIQITFERG 95
 DB 42 ESNHLLDLIRRETTIOVKNGYVOSPRFNYSYPRNLLTLWRHS-QENTRIQIVPNOG 100
 QY 96 LEDPEDDICKYFVEVEEPPSDSVL--GRMGSGTVPKGKOTSGNHIRIRFVSDYFPE 153
 DB 101 LEEAENDIRYFVEVEDSETSTIIRGMCGHKEVPPRIKSTNOKITFEKSDYFAVK 160
 QY 154 PGFCIHYSII--MPQVETT-----SPSVLPSSLSIDLNNAYTAFT 195
 DB 161 PGFKIYYSLEDFQPAASSETNWEVSTSSISGYSNPSVTPD-TLIDALDKIAEFD 219
 QY 196 LBEILRYLEPDMQVLDLSKYPTWOLKAPLYGKSKVYNLILKEEVKLYSCTPRNF 255
 DB 220 VEDLLKYPFESWQEDLENMYLDTPRYGRSY-HDRKSK-VLDRLINDAKRYSCTPRN 277
 QY 256 SVSIREELKRTDTIWPGLLVKRCGNCACCLHNCNEGCYPRKVTKKYHEVLDLRP-- 313

DB 278 SVNIREELKANVAFPRCLLYVRCGNGCGTVMNRSTCNSGKTVKKYHEVLDLRP 337
 QY 314 -KTGVGKLKSLTDVALHEHNEEDCYC 339
 DB 338 IKRRGAKTMAVLDQLDHHERCDCIC 364
 RESULT 9
 ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
 AC Q9BWV5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Iris-expressed growth factor short form.
 GN IEGF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=IRIS;
 RA Wistow G.;
 RT "Iris-expressed Growth Factor (IEGF).";
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 CUB-DOMAIN.
 DR EMBL: AY027518; AAK20082.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR InterPro: IPR000531; TonB_boxc.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 DR SEQUENCE 364 AA; 42166 MW; 245C5358DEA3EAC CRC64;
 SQ

Query Match 40.6%; Score 750.5; DB 4; Length 364;
 Best Local Similarity 45.6%; Pred. No. 4.9e-61;
 Matches 145; Conservative 58; Mismatches 86; Indels 27; Gaps 8;

QY 45 RHRYVITISNGSIHSPKPPHYPRNMVLYRLVAVDENRIQITFERGLEDPEDD 104
 DB 45 RDETTIOVKNGYVOSPRFNYSYPRNLLTLWRHS-QENTRIQIVPNOGFGLEAENDIC 103
 QY 105 KYDFVEVEEPPSDSVL--GRMGSGTVPKGKOTSGNHIRIRFVSDYFPEPGFCIHYST 162
 DB 104 RIDVEVEDSETSTIIRGMCGHKEVPPRIKSTNOKITFEKSDYFAKPGFKIYSL 163
 QY 163 I--MPQVETT-----SPSVLPSSLSIDLNNAYTAFTLEELRYLE 204
 DB 164 LEDFQPAASSETNWEVSTSSISGYSNPSVTPD-TLIDALDKIAEFDYVLDLAKYTN 222
 QY 205 PDRMVDLSLYKPTWOLKAPLYGKSKVYNLILKEEVKLYSCTPRNFVSIREELK 264
 DB 223 PESWQEDLENMYLDTPRYGRSY-HDRKSK-VLDRLINDAKRYSCTPRNYSVIREELK 280
 QY 265 RDTIWPGLLVKRCGNCACCLHNCNEGCYPRKVTKKYHEVLDLRP--KTGKGLH 321
 DB 281 LANVAFPRCLLYVRCGNGCGTVMNRSTCNSGKTVKKYHEVLDLRPFGHILRRGAKT 340
 QY 322 KSLTDVALHEHNEEDCYC 339
 DB 341 MALVVDIQLDHHERCDCIC 358
 RESULT 10
 ID Q92517 PRELIMINARY; PRT; 370 AA.
 AC Q92517;

RC	STRAIN=C57BL/6J; TISSUE=EMBRO.
EX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA	Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiwa H.,
RA	Knehl P., Lewis S., Matsuo Y., Nikido I., Pesole G., Quackenbush J.,
RA	Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustlich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazerelli J., Monbaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
RA	wysshaw-booris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR	EMBL: AK003359; BAB22733.1; -;
DR	MGD: MGI:1919035; Pdgfg.
DR	InterPro: IPR000859; CUB_domain.
DR	InterPro: IPR000072; PD_growth_factor.
DR	Pfam: PF00431; CUB. 1.

DR SMART; SM00141; PDF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDF_2; 1.

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Query Match      35.7%; Score 660; DB 11; Length 290;
Best Local Similarity 46.6%; Pred. No. 8,5e-53;
Matches 131; Conservative 48; Mismatches 76; Indels 26; Gaps
QY      82  ENVNLTLPFERFEGLEPEDDICKYDFEVEEEDSDGS--VLGRMGSGSTVPGRKQTSKGNH 139
      |  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      7  EKTQIQLSFHQFGLFPAENDICRYDFEVEEYESSESTVGRMGCGKREIPITTSRTNO 66
QY      140  IRIEVEDEVEPSPGHCISYII---MPQVTEY-----SPKVLPPSS 181
      |  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      67  IKITFKSDDDIVAAPEGRKIITYEVEDFQPPASSETMNESSTSSFGVSYHSITDP-7L 125
QY      182  SLDLNNAAVTAFTLEELIYLEEDRWQVLDLSLYKPTWOLLKAEFLGKRKSRYVNLNL 241
      |  | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      126  TADVLDTVAEFDVEEDLLKHNPNVSMODOLENLYLDTPIYRGRSY-HDRKS-VLDRL 183
QY      242  KEVKLYLSCGPRNVSYSIREELKRTDPIIPGGLLYKRGCGNACCLHNNEGCVPRRY 301
      |  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      184  NDDVKRISCTPRNHSVNLREELKILTNVFFPRCLLYVORCGNCGCGTVMKSCSTCGSXT 243
QY      302  TKKYHEVLTLP---KTGVGLKSLKSLTDVALHNNEEDCG 339
      |  ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | :

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RESULT 12
Q80FX6
AC Q80FX6; PRELIMINARY; .PRT; 923 AA.
DT 01-JUN-2002 (TREMBLrel. 2i, Created)
DT 01-JUN-2002 (TREMBLrel. 2i, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 2i, Last annotation update)
DE Neurofilin-1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]_TAN
IN

```



```

CC -! SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL; D83476; BAA11922.1; -.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.005; -.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000130; Zn_MTEptidse.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 977 AA; 110199 MW; 4D7D2E37C64FDF1F CRC64;

Query Match 10.3%; Score 191; DB 13; Length 977;
Best Local Similarity 45.2%; Pred. No. 1e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSKFPHTIPRNVLVRLVAVDENVRIOLEPDERFGLDEPDIDICKYDFVEVEE- 113
   |||::||:| || |::||| |::||| |::||| |::||| |::||| |::||| |::|||
Db 590 NGSIINSPGWPEKPPNKNCIWQIVAPTO-YRISLKFDO---FETEGNDVCKYDFVEVRSG 645

QY 114 -PSDGSVLGRMGSGTVPGKOTSKGNHRIREFVSDSEYFSPSPGF 156
   || : |::||| |::||| |::||| |::||| |::||| |::||| |::|||
Db 646 LTSDSKLHGKFCGS-ELPAVITISQYNNNRIFEFKSDNTV-SKKG 687

```

Search completed: April 29, 2003, 09:08:09
 Job time : 56 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:11 ; Search time 15.5 seconds
(without alignments)
2139.766 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLLTSAAGQRTGT.....DVALEHHEECDCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	40.8	370	2 JC7592	spinal cord-deri
2	753	40.7	370	2 JC7591	spinal cord-deri
3	191	10.3	707	2 JC2218	procollagen C-endo
4	190	10.3	823	1 A58788	procollagen C-endo
5	183.5	9.9	730	1 BMH01	procollagen C-endo
6	183.5	9.9	927	1 J00948	A5 antigen precurs
7	181	9.8	986	1 B58788	procollagen C-endo
8	181	9.8	991	2 I48540	procollagen C-endo
9	174.5	9.4	3623	2 T09456	Intrinsic factor-B
10	160	8.7	3623	2 T08618	Intrinsic factor-B
11	158	8.5	449	2 A55362	procollagen I C-pr
12	153	8.3	1057	1 A39288	dorsal-ventral pat
13	147.5	8.0	1524	2 T30337	polypeptide - Afri
14	145.5	7.9	686	1 A59271	Ra-reactive factor
15	144	7.8	699	1 I54763	Ra-reactive factor
16	143.5	7.7	597	2 S71352	metalloproteinase
17	141.5	7.7	1070	2 T31069	collagen-BMP-1 like
18	140.5	7.6	3871	2 T32812	hypothetical prote
19	139	7.5	1594	2 T30549	hensin - rabbit
20	137.5	7.4	705	1 C1HUR8	complement subcomp
21	135.5	7.3	1464	2 S58984	development protei
22	133.5	7.2	402	2 JH0403	procollagen I C-pr
23	128	6.9	277	2 A41735	hyaluronate-bindin
24	127	6.9	419	2 S69207	vascular endotheli
25	126.5	6.8	579	2 JCT629	membrane-type friz
26	125.5	6.8	245	1 TVCTSS	platelet-derived g
27	125.5	6.7	767	2 T30018	hypothetical prote
28	123	6.7	275	2 J06506	tumor necrosis fac
29	122.5	6.6	2403	2 A59386	sanko - human

30	119.5	6.5	2083	2 T42721	CRP-ductin-alpha p
31	117.5	6.4	276	2 A47290	TSG-6 homolog p54
32	117.5	6.4	1290	2 A57190	ebnerin precursor
33	114.5	6.2	200	2 I51551	platelet-derived g
34	114.5	6.2	215	2 S08220	platelet-derived g
35	114.5	6.2	226	2 I51550	platelet-derived g
36	113	6.1	695	1 S05008	complement subcomp
37	112.5	6.1	241	1 PFH0G2	platelet-derived g
38	111.5	6.0	226	1 TVMYS5	PDGF-related trans
39	109	5.9	694	2 JC6554	complement subcomp
40	108.5	5.9	148	2 D49530	16k vascular endot
41	107	5.8	321	2 T33161	hypothetical prote
42	104	5.6	319	2 I51569	UVS-2 protein - Af
43	103.5	5.6	225	2 S25097	platelet-derived g
44	103	5.6	196	2 B28964	platelet-derived g
45	103	5.6	211	1 PFH0G1	platelet-derived g

ALIGNMENTS

RESULT 1

JC7592
spinal cord-derived growth factor-B precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #ext_change 24-Aug-2001

C:Accession: JC7592

R:Hamada, T.: Ut-Tel, K., Imaki, J., Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCGF-B, a novel growth factor homologous to SCDF/PDGF

A:Reference number: JC7591; MUID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: JC7592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-references: DDBJ:AB052170

C:Gene(s):

A:Gene: scdgrf-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:32-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial g

F:294-308/Region: conserved motif #status predicted

Query Match 40.8%; Score 754; DB 2; Length 370;

Best Local Similarity 46.2%; Pred. No. 1.4e-55;

Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

QY	37	EQNGVOD-PHERVVRITSGNSIHSPKFPHTYPRNMVLYVAVDENVRIOITFDERFG	95
DB	42	ESNHLIDLYRDEIRKRTGTHGVQSPFPNSYPRNLLTRKLS-QKTRIQALAFDHFQ	100
QY	96	LEDDPDDICKYDFEVEEPESDGS--VLGRWGSQTYVGKOTSKGNHRIKRVSDPEPSE	153
DB	101	LEAENDICRYDFEVEEDVSESSYVGRWCGHKEIPRTSRNQIKITFOSDDYVAK	160
QY	154	PGGCIHSHII---MPQ-----VRET-----TPSVLPSSSLDILNNAVTFST	195
DB	161	PGFTYISFVEDPQPEASSEIMESVTSFSGVSYHSPVW-BSTLPAADLADNAIEFD	219
QY	196	LEELIRYLEPDRMOVDLSYKPTMQLGKAFYLGKSKVNNLKEEYKLSCTPRNF	255
DB	220	VEDLTKKFNASMOVDLENLYMDTPRRGRSY-HERSK-VDDRLNDVYKRSCTPRNH	277
QY	256	SVSIREPLKRTDTITFMGCLLVKRCGNCACCLHNCNCCVPRKYKKYHEVQLRP--	313
DB	278	SVNIREPLKLTNAVFFPRCLLVORCGNCGGLTNMKSCTSSGKTVKKYHEVLEKPRGH	337
QY	314	-KTVGKGLHSKLDVALEHHEECDCVC	339
DB	338	FKRGRKAKMALVDYDQDHHERCDCIC	364

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RESULT 2
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7591
R:Hamada, T.; Ue-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDEF/C/
A:Reference number: JC7591, MUID:21092670, PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-References: DDBJ:AB033832
C:Genetics:
A:Gene: scdgf-B
F:1-17/Domain: secretory signal sequence #status predicted <STG>
F:18-170/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

```

```

Query Match      40.7%: Score 753; DB 2: Length 370;
Best Local Similarity 45.3%: Pred. No. 1.7e-55;
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

OY 37 EONGYOD--PRHRRVYVTSIGNGSIHSPKFPHTYPRRMVLRVLRVAVDENVRIQLTFDEDFEG 95
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |
Db 42 ESNHLLTLRLRREFITQVGVNGCYVSPRPNFSYPRNLLLTWRHS-QENTRIQLDYFDNFG 100
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |

OY 96 LEDPDDICKYDFVEVEEBSDGSVL--GRWCGSGTVPEKQTSKGNHIRIYVSDYEPSE 153
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |
Db 101 LEEANDICRYDFVEVEDISFETSTIIRGRCMGHKEVPRIKSRITQIKITFSDSYFAVK 160
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |

OY 154 PGFCIHYSI---MQVYETT-----SPSVLPSSLSLDLNNATAST 195
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |
Db 161 PGFKYIVSLLEDFOPAAASSETMWSVTSISGSVSNSSVYDP--TLIDALDLPKKAEDT 219
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |

OY 196 LELLIRYLEPRDQVODLSLYKPTWQLGKAFLYGGKSKVVNLNLKEEVLKYSTCPRNF 255
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |
Db 220 VEDLLKTYNPEBQMDLLENMYLDLTRYGRGRY-HSRKSK-VDLIDLNDARKRYSTCPRNY 277
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |

OY 256 SVSIREELKRIDTIFWPGCLLYKRCGNCACCLHNCNECCQVPRRYTKYHNEVLQLRP-- 313
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |
Db 278 SVNIEELKLAIVYFFPRCLLVQRCGNGCGCTVMMRSCTCSGTVAKKYHNEVLQFERGH 337
      | | | | | : : : : : | | | | | : : : : : | | | | | : : |

OY 314 -KTGVKGLHSLTDVALEHNEBCDVC 339
      | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 338 IKRRGRATMALVYDLDHNERCDIC 364
      | : : : : | : : : : | : : : : | : : : : | : : : : |

```

RESULT 3
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N:Alternate names: bone morphogenic protein 1
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C:Accession: JC2218
R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A:Title: Cloning and expression of cDNA encoding *Xenopus laevis* bone morphogenetic protein
A:Reference number: JC2218; MID:J94085787; PMID:826384
A:Accession: jc2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: GB:LI2249; MID:9406540; PIDN:AAA16313.1; PID:9406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; asctsin homology; Clr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
E:93-284/Domain: asctsin homology <ASST>
E:285-397/Region: complement I/r/I5-like repeat
E:285-394/Domain: Clr/Cls repeat homology <CLR1>
E:398-510/Region: complement I/r/I5-like repeat

```
F:398-507/Domain: C1r/C1s repeat homology <C1R2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: Complement Irf1S-like repeat
F:554-663/Domain: C1r/C1s repeat homology <C1R3>
F:62,109,295,336/Binding site: carboxylate (Asn) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match      10.3%: Score 191; DB 2; Length 707;
Best Local Similarity 45.2%; Pred. No. 6.7e+08;
Matches   47; Conservative    16; Mismatches   33; Indels     8; Gaps     5;
```

RESULT 4
A:58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278, A58788
R:Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:9072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'ERRPALQPPGRPHQLKFRVQKRNRTPQ' <MOZ>
A:Cross-references: GB:422488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (mTld) are en
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TKA>
A:Cross-references: GB:I35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
C:Genetics:
A:Gene: GDB:BMP1, BMP-1
A:Cross-references: GDB:I125203; OMIM:112264
A:Map position: 8p21-8p21

[illegible]

GenCore version 5.1.4-P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 08:58:01 ; Search time 9 Seconds
(without alignments)
1589.926 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MULTISUBSEQUENCE.....DVALHHEEDCVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	10.3	707	1	BMPL_XENLA
2	183.5	9.9	928	1	NRPL_XENLA
3	181	9.8	986	1	BMPL_HUMAN
4	181	9.8	991	1	BMPL_MOUSE
5	176	9.5	923	1	NRPL_HUMAN
6	174	9.4	1022	1	TLD_BRARE
7	172	9.3	922	1	NRPL_RAT
8	169	9.1	923	1	NRPL_MOUSE
9	167	9.0	914	1	NRPL_CHICK
10	163.5	8.8	616	1	SPAN_STRPU
11	158	8.5	449	1	PCOI_HUMAN
12	155.5	8.4	925	1	NRPL_MOUSE
13	155.5	8.4	931	1	NRPL_RAT
14	155.5	8.4	931	1	NRPL_MOUSE
15	153.5	8.3	326	1	VEGD_RAT
16	153	8.3	1057	1	TLD_DROME
17	147.5	8.0	704	1	CRAR_MOUSE
18	145.5	7.9	686	1	MAST_HUMAN
19	144.5	7.8	597	1	BP10_PARKI
20	144	7.8	699	1	CRAR_HUMAN
21	137.5	7.4	705	1	CIR_HUMAN
22	136.5	7.4	468	1	PCOI_RAT
23	136	7.4	354	1	VEGD_HUMAN
24	135.5	7.3	358	1	VEGD_MOUSE
25	133.5	7.2	468	1	PCOI_MOUSE
26	132	7.1	415	1	VEGD_MOUSE
27	130	7.0	639	1	BMPL_STRPU
28	128	6.9	1	1	TSBG_HUMAN
29	127	6.9	419	1	VEGD_HUMAN
30	125.5	6.8	245	1	PDGB_FELCA
31	123	6.7	275	1	TSBG_MOUSE
32	117.5	6.4	276	1	TSBG_RABIT
33	114.5	6.2	226	1	PDGA_XENLA

34	113	6.1	695	1	CASP_MESAU
35	112.5	6.1	241	1	PDGB_HUMAN
36	111.5	6.0	164	1	VEGA_CAVPO
37	111.5	6.0	226	1	TSIS_SMSAV
38	109	5.9	855	1	ST14_HUMAN
39	108.5	5.9	148	1	VEGD_ORFN7
40	105.5	5.7	207	1	VEGD_HUMAN
41	104	5.6	514	1	UVS2_XENLA
42	103.5	5.6	207	1	VEGD_BOVIN
43	103.5	5.6	225	1	PDGB_RAT
44	103.5	5.6	241	1	PDGB_SHEEP
45	103	5.6	211	1	PDGA_HUMAN

ALIGNMENTS

RESULT 1	BMPL_XENLA	STANDARD:	PRT:	707 AA.
ID	BMPL_XENLA			
AC	P98070:			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RA	MEDLINE=94085767; PubMed=8262384;			
RA	Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;			
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone			
RT	morphogenetic protein-1 during early embryonic development."			
RL	Gene 134:257-261(1993).			
CC	- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER			
CC	DIFFERENTIATION OF DEVELOPING ORGANS.			
CC	- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED			
CC	TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.			
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.			
CC	- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
CC	- SIMILARITY: CONTAINS 3 CUB DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L12249; AAA16313.1; -			
DR	HSSP; P00736; IAP0.			
DR	MEROPS; M12.005; -			
DR	InterPro; IPR001506; Astacin.			
DR	InterPro; IPR000152; Asx_hydroxyl.			
DR	InterPro; IPR000859; CUB-domain.			
DR	InterPro; IPR000561; EGF-like.			
DR	InterPro; IPR001881; EGF Ca.			
DR	InterPro; IPR000130; zn_MTPpeptidase.			
DR	Pfam; PF00008; EGF_1.			
DR	Pfam; PF00431; CUB; 3.			
DR	Pfam; PF01400; Astacin; 1.			
DR	PRINTS; PR00480; ASTACIN.			
DR	SMART; SM00042; CUB; 3.			
DR	SMART; SM00179; EGF_CA; 1.			
DR	SMART; SM00235; ZINC; 1.			
DR	SMART; PS00142; ZINC_PROTEASE; 1.			
DR	PROSITE; PS01180; CUB; 3.			
DR	PROSITE; PS001010; ASX_HYDROXYL; 1.			

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DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
KW Growth factor: Cytokine; Repeat: Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 83 ? POTENTIAL.
FT CHAIN 84 707 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 84 284 METALLOPROTEASE.
FT DOMAIN 285 397 CUB 1.
FT DOMAIN 398 509 EGF_2.
FT DOMAIN 510 551 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 554 666 CUB 3.
FT METAL 176 176 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 177 177 BY SIMILARITY.
FT METAL 180 180 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 535 BY SIMILARITY.
FT CARBOHYD 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC98BD CRC64;

Query Match 10.3%; Score 191; DB 1; Length 707;
Best Local Similarity 45.2%; Pred. No. 5; 1e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHPTPRNMVLVRLVAVDENVRITQLTDFERFGLDEPEDDICKYFVEE- 113
DB 562 NGSIHSPKPHPTPRNMVLVRLVAVDENVRITQLTDFERFGLDEPEDDICKYFVEE- 113
DB 562 NGSIHSPKPHPTPRNMVLVRLVAVDENVRITQLTDFERFGLDEPEDDICKYFVEE- 113
QY 114 -PSDGSVLRGMSGTVPGKOTSGKNHRIKRVSDYFSEPGF 156
DB 618 LTFSDSKLHGKFGCS-ELPAVITSGYNNMRLEPKSDNTV-SKKGF 659

RESULT 2
ID NRPL_XENLA STANDARD; PRT; 928 AA.
AC P28824;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-1 precursor (A5 protein) (A5 antigen).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91337458; Pubmed=1908252;
RA Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
RT "The A5 antigen, a candidate for the neuronal recognition molecule,
has homologues to complement components and coagulation factors.";
RL Neuron 7:295-307(1991).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CERAMIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION
BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
NEURONS.
CC -1- SIMILARITY: BELONGS TO THE NEUPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

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CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
-----
CC EMBL: D10467; BAA01260.1; -.
CC HSSP: P12259; 1CZT.
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; FA5B.C.
CC InterPro: IPR000998; MAM_domain.
CC Pfam: PF00431; CUB; 2.
CC Pfam: PF00629; MAM; 1.
CC Pfam: PF00754; F5_F8_Type_C; 2.
CC PRINTS: PR00020; MAMDOMAIN.
CC SMART: SM00042; CUB; 2.
CC SMART: SM00331; FA5B.C; 2.
CC SMART: SM00137; MAM; 1.
CC PROSITE: PS00740; MAM_1; 1.
CC PROSITE: PS01180; CUB; 2.
CC PROSITE: PS01285; FA5B.C; 1; 2.
CC PROSITE: PS01286; FA5B.C; 2; 2.
CC PROSITE: PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neuron; Signal; Repeat; Receptor;
KW Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 928 NEUPILIN-1.
FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 861 883 POTENTIAL.
FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 584 F5/8 TYPE C 2.
FT DOMAIN 646 812 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 584 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 928 AA; 103416 MW; AFB323B0A4CT89D CRC64;

Query Match 9.9%; Score 183.5; DB 1; Length 928;
Best Local Similarity 30.7%; Pred. No. 2; 9e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

QY 50 VTIHSGNSIHSKPHPTPRNMVLVRLVAVDENVRITQLTDFERFGLDEPEDDICKYFV 109
DB 31 KITSPSYLTSAGIPHYPSQRCWELQPEHYQRTMINFNHFDLEDE---CRYDIV 87
QY 110 EV--EERPSDGSVLRGMSGTVPGKOTSGKNHRIKRVSDYFSEPGFICFIHSIIM--P 165
DB 88 EVIDGDANAGQLGKCYGK-IAPSPLYSTPSPSIFIRVSDYFEPG-AGSIRIVRYKTPG 145
QY 166 QVTE--TTPSVLP-----PSSLSDLLNNAVTAFTLEELIRYLEPDRMQVDLS 214
DB 146 ECSRNFSSNGSIKSPKPYPEKYNALCTYIIIPA---PKMQRTV--LEEFSEFLADS 198

RESULT 3
ID BMPL_HUMAN STANDARD; PRT; 986 AA.

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DB 660 LPAADSLHKGFCGS-EKPEVITSQYNNMRYEKFSDNTV-SKNGKFAHF 705

RESULT 5

NRPI_HUMAN STANDARD: PRT; 923 AA.

ID NRPI_HUMAN 060461;

AC 014786; 060461;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Neupoplin-1 precursor (Vascular endothelial cell growth factor 165 receptor).

GN NRPI OR NRP OR VEGF165R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RA (1)

RP SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM).

RX MEDLINE=97433084; PubMed=9288753;

RT He Z., Tessier-Lavigne M.;

RT "Neuropilin is a receptor for the axonal chemorepellent semaphorin III.";

RT Cell 90:739-751(1997).

RL (2)

RN SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39.

RP TISSUE=Breast;

RX MEDLINE=98188099; PubMed=9529250;

RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;

RT "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";

RT Cell 92:735-745(1998).

RL (3)

RN SEQUENCE FROM N.A. (SOLUBLE/SNRPI ISOFORM), AND SEQUENCE OF 22-31.

RP TISSUE=Prostatic adenocarcinoma;

RX MEDLINE=20183929; PubMed=1068880;

RA Gagnon M.L., Bieleberg D.R., Gschman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.;

RT "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).

RL (4)

RN CHARACTERIZATION.

RP MEDLINE=20309748; PubMed=10748121;

RA Gluzman-Poltorak Z., Cohen T., Hertzog Y., Neufeld G.;

RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of Placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";

RT J. Biol. Chem. 275:18040-18045(2000).

RL (5)

RN FUNCTION: THE MEMBRANE-BOUND ISOFORM IS A RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOPUSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS.

CC -1- FUNCTION: THE SOLUBLE/SNRPI ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRPI ISOFORM IS SECRETED.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: MEMBRANE-BOUND (SHOWN HERE) AND SOLUBLE/SNRPI. ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND SOLUBLE/SNRPI ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT

CC TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART AND PLACENTA. MODERATELY IN LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS. AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRPI ISOFORM IS FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.

CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.

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CC -----

CC EMBL: AF018956; AAC51759.1; -

CC EMBL: AF016050; AAC12921.1; -

CC EMBL: AF145712; AAF4344.1; -

CC HSSP: P12259; 1CZ7.

CC GeneW: HGNC:8004; NRPI.

CC MIM: 602069; -

CC InterPro: IPR000859; CUB_domain.

CC InterPro: IPR000421; FASB_C.

CC InterPro: IPR001092; HLH_Basic.

CC InterPro: IPR000998; MAM_domain.

CC Pfam: PF00431; CUB; 2.

CC Pfam: PF00629; MAM; 1.

CC Pfam: PF00754; F5_F8_type_C; 2.

CC PRINTS: PR00020; MAMDOMAIN.

CC SMART: SM00042; CUB; 2.

CC SMART: SM00231; FAS8C; 2.

CC SMART: SM00137; MAM; 1.

CC PROSITE: PS01180; CUB; 2.

CC PROSITE: PS01285; FAS8C_1; 2.

CC PROSITE: PS01286; FAS8C_2; 2.

CC PROSITE: PS00740; MAM_1; 1.

CC PROSITE: PS50060; MAM_2; 1.

CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;

KW Alternative splicing.

FT FT SIGNAL 1 21

FT CHAIN 1 923

FT DOMAIN 22 923

FT TRANSMEM 857 856

FT DOMAIN 857 879

FT DOMAIN 923 923

FT DOMAIN 27 141

FT DOMAIN 147 265

FT DOMAIN 275 424

FT DOMAIN 431 583

FT DOMAIN 443 811

FT DISULFID 27 54

FT DISULFID 82 104

FT DISULFID 147 173

FT DISULFID 206 228

FT DISULFID 275 424

FT DISULFID 431 583

FT CARBOHYD 150 150

FT CARBOHYD 261 261

FT CARBOHYD 300 300

FT CARBOHYD 522 522

FT CARBOHYD 842 842

FT VARSPLC 642 644

FT VARSPLC 645 923

FT CONFLICT 26 26

FT CONFLICT 749 749

FT CONFLICT 855 855

SO SEQUENCE 923 AA; 103120 MW; ADEADCA4A95ED57 CAC64;

Query Match 9.5%; Score 176; DB 1; Length 923;

Best Local Similarity 32.6%; Pred. No. 1,2e-06;

Matches 57; Conservative 24; Mismatches 68; Indels 26; Gaps 9;

OY 50 V[ISNGS]HSHKPHPTYYRNNVLWRLVAVDENWVLTOLTPEREGLDEPDIDKCYDEV 109
 Db 31 I[IESBPGY]LTS[CGY]HSHYSEKCEMLIADPDYORIMINFNHPLELDRD---CAYDV 87
 OY 110 EV--E[EPSD]SVLGRMCGSGTVP[CGK]OTSKGNHIRIRFVSEDEYFPSPGFCIHYSITM--P 165
 Db 88 E[VDENENEN]GHRFGKFCGK-IAPPPVSSGPFLEIKFVSD-YETHAGSIRIREIKRRP 145
 OY 166 QVTE--T[TS]PSVLP-----P[SS]LSDLLNNAVTAFTLEELIRY----LEPD 206
 Db 146 E[CSQNTVTP]SGVYKISGPEPKYNSLECTYI--VFAPRMS[ET]ILEFESFDLEPD 197
 RESULT 6
 TLD_BRARE
 ID TLD_BRARE STANDARD: PRT: 1022 AA.
 AC 057460.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
 DE (mini fin protein).
 DE TOLOID OR TLD OR MEN.
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX Nchi_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Gastrula;
 RX MEDLINE=98057457; PubMed=9395394;
 RA Blader P., Rastegar S., Fischer N., Strengle U.;
 RT "Cleavage of the BMP-4 antagonist chordin by zebrafish Tollid.";
 RL Science 278:1937-1940(1997).
 RN [2]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=99307076; PubMed=10375503;
 RA Connors S.A., Trout J., Ekker M., Mullins M.C.;
 RT "The role of tollid/mini fin in dorsoventral pattern formation of the
 RT zebrafish embryo.";
 RL Development 126:3119-3130(1999).
 CC -I- FUNCTION: Required for patterning ventral tissues of the tail. May
 CC increase bone morphogenetic protein (BMP) activity at the end of
 CC gastrulation by proteolytic cleavage of chordin and release of BMP
 CC from inactive complexes.
 CC -I- TISSUE SPECIFICITY: During gastrulation, accumulates around the
 CC closing blastopore with greater expression ventrally. At the
 CC animal pole, expressed in the ectoderm flanking the anterior
 CC neural plate. At the 10-somite stage, expressed in the developing
 CC tailbud and cranial neural crest. At the 20-somite stage, also
 CC expressed in the hematopoietic system.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -I- SIMILARITY: CONTAINS 5 CUB DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF027596; AAC60304.1; -
 DR HSSP: P35553; IEMN.
 DR MEROPS: M12.016; -
 DR ZFIN: ZDB-GENE-990415-265; tolloid.
 DR InterPro: IPR001506; Astacin.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000859; Cub_domain.
 DR InterPro: IPR000561; EGF-like.

Query Match	Best Local Similarity	Score 174:	DB 1:	Length 1022:
Matches 45; Conservative 20; Mismatches 35; Indels 8; Gaps 6;				
QY 55	NGSINSPKPEHTYPRNNWLVNRLVAVDENVRITQLTFDFRFGLEDEDDICKYFVEVEE- 113			
DB 635	NGTITTPMPKREYEPKNNKCMQVAPQ-YRISMGF-EAFLEEG-NEWCKYDYEVASG 690			
QY 114	-PSDGSVGRMCQSGCTVPGKOTSKSNHRIKRFVSDYETPPSEGGCITHY 160			
DB 691	LSSDSKLGKYGCGT-EVPEVITSTQYNNNRRIEKSQNTNT-SKKGEFAHF 736			

RESULT 7
 NRPL_RAT STANDARD: PRT: 922 AA.
 AC 090009: 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
 GN NRPL.
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97433085; PubMed=9288754;
 RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J., Ginty D.D.;
 RL "Neuropilin is a semaphorin III receptor."
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOREGULATION OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A. THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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 CC -----
 DR EMBL: AF016296: AAC53337.1: -
 DR HSPF: P12259: IC2T.
 DR InterPro: IPR000859: CUB_domain.
 DR InterPro: IPR000421: FA58_C.
 DR InterPro: IPR001092: HLH_basic.
 DR InterPro: IPR000998: MAM_domain.
 DR Pfam: PF00431: CUB; 2.
 DR Pfam: PF00629: MAM; 1.
 DR Pfam: PF00754: F5_F8_type_C; 2.
 DR PRINTS: PR00020: MAMDOMAIN.
 DR SMART: SM00042: CUB; 2.
 DR SMART: SM00231: FA58C; 2.
 DR SMART: SM00137: MAM; 1.
 DR PROSITE: PS01180: CUB; 2.
 DR PROSITE: PS01285: FA58C_1; 2.
 DR PROSITE: PS01285: FA58C_2; 2.
 DR PROSITE: PS00740: MAM_1; 1.
 DR PROSITE: PS00600: MAM_2; 1.
 DR Transmembrane: Glycoprotein; Neurone; Signal; Repeat; Receptor.
 FT SIGNAL 1 21
 FT CHAIN 1 21
 FT DOMAIN 22 922
 FT TRANSMEM 856 855
 FT DOMAIN 881 922
 FT DOMAIN 881 922
 FT DOMAIN 141 141
 FT DOMAIN 147 265
 FT DOMAIN 275 424
 FT DOMAIN 431 583
 FT DOMAIN 431 583
 FT F5/8 TYPE C 1.
 FT F5/8 TYPE C 2.

FT DOMAIN 645 811 MAM.
 FT DISULFID 27 54 PROBABLE.
 FT DISULFID 82 104 PROBABLE.
 FT DISULFID 147 173 PROBABLE.
 FT DISULFID 206 228 PROBABLE.
 FT DISULFID 275 424 BY SIMILARITY.
 FT DISULFID 431 583 BY SIMILARITY.
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 922 AA: 103082 MW: CC6F82AD098B0F2E CRC64;
 Query Match 9.3%; Score 172; DB 1; Length 922;
 Best Local Similarity 31.5%; Pred. No. 2.5e-06;
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
 QY 2 LLLGLLLTSLALGQRTGTRAESNLSSKLLQSSDKQNGVQDPRHRRVYITSGNSIHSF 61
 DB 7 LCATLALALALAG-----AFRSKCGG-----TIKENPGYLTSP 42
 QY 62 KPPPTPRNVLVWRLVAVDENVRQLTDERPGLDEPDDICKYDFVEY--EPPSDGSV 119
 DB 43 GYPHSYSPSKCEMLIQAEPPYRIMINPHDLEDRD---CKYDYVEIDENGSGRL 99
 QY 120 LGWCGSGYTPGKQTSKGNIRIRFVSDEFSPSPFCIHYSIIM--PQTER-TSPS 174
 DB 100 WGFEGCK-IAPSPVSSGPLELTFKFSVD-YETHGAGSIRYELFKRQSPCSQNTAPT 155
 RESULT 8
 NRPL_MOUSE STANDARD: PRT: 923 AA.
 ID NRPL_MOUSE
 AC P97333:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropilin-1 precursor (A5 protein).
 GN NRPL OR NRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C; TISSUE=Embryonic brain;
 RX MEDLINE=96353149; PubMed=8748368;
 RA Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;
 RT "Developmentally regulated expression of a cell surface protein, neuropilin, in the mouse nervous system."
 RL J. Neurobiol. 29:1-17(1996).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOREGULATION OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A. THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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```

Matches      51: Conservative       31: Mismatches       65: Indels       30: Gaps
QY          50 VTISGNSIHSPKRPHTYPRMMVLVRLVAVDENVRIQLTDFDERGLDEDPEDICKYDFV 109
              : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db          29 IKILSPCLITSPGYPOSYPHPSOKCEMLIOAPEPPYORIMINPNHPDLERD---CKDYDV 85
QY          110 EV--EEPDSGVLCWMCSSGTVPKQTSKGNIIRFRPVSDEFPEEPGPCIHYSLIM--P 165
              || : : : : | : ||| | | : : : : | : ||| | | : : : : | : ||| | | : : : :
Db          86 EVIDGDNAEGRMGMKYCK -IAPPLVSSGGYLFTKFVSD-YETHAGSINLEYEFKKCP 143
QY          166 QVTE-TPSPSVLP-----PSSLSDL-----LNNVAFASTLEELLRYLPLED 206
              : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db          144 ECSRNFTSSSGMINSPPGEKYPNLSLECTYIIIFAKMEIILFEFSFE----LEPD 195

RESULT 10
SPAN_STRPU
AC SPAN_STRPU STANDARD; PRT; 616 AA.
P98068:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SPAN protein precursor (EC 3.4.24.*.)
GN SPAN.
OS Strongylocentrotus purpuratus (Purple sea urchin)
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
OX Strongylocentrotus.
XX NCBI_TaxID=7668;
RN [1]
RM SEQUENCE FROM N.A.
RX MEDLINE=92315921; PubMed=1618141;
RA Reynolds S.D., Angerer L.M., Palls J., Nasir A., Angerer R.C.;
RT "Early mRNAs, spatially restricted along the animal-vegetal axis of
RT sea urchin embryos, include one encoding a protein related to tollid
RT and BMP-1."
RL Development 114:769-786(1992).
CC -!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
CC -!- OF THE BLASTULA.
CC -!- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
CC AND HATCHING).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -----
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CC -----
DR EMBL; M84144; AAA30072.1; -.
DR HSP; P28825; ITAF.
DR MEROPS; M12_013; -.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000130; Zn_MTpeptidse.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF01400; Astacin; 1.
DR PRINTS; PRO0480; ASTACIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00235; Zmnc; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
KW Developmental protein; Repeat; Hydroxylase; Protease; zinc; Embryo;
KW Metalloprotease; Egf-like domain; Signal.
FT SIGNAL
   1
   16
   POTENTIAL.

```

FT	PROPEP	17	93	ACTIVATION PEPTIDE (POTENTIAL)
FT	CHAIN	94	616	SPAN PROTEIN.
FT	DOMAIN	89	93	ARG/LYS-RICH (BASIC).
FT	DOMAIN	94	295	METALLOPROTEASE.
FT	DOMAIN	295	329	EGF-LIKE.
FT	DOMAIN	450	450	CUB 1.
FT	DOMAIN	341	502	THR-RICH.
FT	DOMAIN	503	614	CUB 2.
FT	METAL	190	190	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE	191	191	BY SIMILARITY.
FT	METAL	194	194	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	200	200	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULFID	299	315	BY SIMILARITY.
FT	DISULFID	305	317	BY SIMILARITY.
FT	DISULFID	319	328	BY SIMILARITY.
SO	SEQUENCE	616 AA:	67902 MM:	397CD923FFB9EB98 CRC64;
Query Match 8.8%; Score 163.5; DB 1; Length 616.				
Best Local Similarity 28.0%; Pred. No. 7.7e-06;				
Matches 63; Conservative 30; Mismatches 86; Indels 47; Gaps 11;				
OY	9	LTSALAGORTG-TRAESNLSKLTQSSDPE-----QNCVQDPRIHRYV--TISGN-55		
DB	269	LSNRL-GORTALSADIELANRIYECDDVEDCSNADCLNGIRHADDCVCPSSYSGLD-327		
OY	56	-----GSHSPKFPPTYPYPRNVLWMLVAVDENVRIQLTFDERF-94		
DB	328	CODGGPTVPADCSYFTFEMTGEITSFNPSPNYEDNTACVYEIEG-PYGSTIELTF--L-383		
OY	95	GLEDPEDDICKDFEVEPEPSSDGVLRGCGSGYPPGKOTSGNRIIRFVSDPEFSP--152		
DB	364	DMEIETELCRDAEAEVRKDDINSIGERCGN-TLPPVQISSNMOMVSTSD---PSIT-439		
OY	153	EEGFCIHYSIIIPQVT--ETTSVSLPSSSLDNLNNAVTFST-195		
DB	440	RGFATFYIIITTTVESTTTLQTTPESTTTLQTTNPSTTTLQTT-484		
RESULT 11				
PCOL_HUMAN		STANDARD:	PRT:	449 AA.
AC	015113:014550:			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-proteinase enhancer protein).			
GN	PCOLCE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=95014462; Pubmed=7523404;			
RA	Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,			
RA	Jani-Sait S., Shows T.B., Greenspan D.S.,			
RT	"Type I procollagen COOH-terminal proteinase enhancer protein:			
RT	identification, primary structure, and chromosomal localization of the			
RT	cognate human gene (PCOLCE)."			
RL	J. Biol. Chem. 269:26280-26285(1994).			
RN	[2]			
RP	REVISIONS TO 56; 154 AND 373.			
RA	Kessler E.;			
RL	Unpublished observations (FEB-2000).			
RN	[3]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RA	Hirahara T., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,			
RA	Morisaki N., Saito Y.;			
RT	"Smooth muscle cell derived procollagen C-protease enhancer protein.;"			

RL Cell Struct. Funct. 21:662-662(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99018118; PubMed-9799793;
 RA Glockner G., Scherer S., Schatkevoy R., Boright A., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RT "Large-scale sequencing of two regions in human chromosome 7q22:
 RT analysis of 650 kb of genomic sequence around the EPO and CUGT1 loci
 RT reveals 17 genes";
 RL Genome Res. 8:1060-1073(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-99134301; PubMed-9933570;
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
 RT "Structural organization and expression patterns of the human and
 RT mouse genes for the type I procollagen COOH-terminal proteinase
 RT enhancer protein";
 RL Genomics 55:229-234(1999).
 RN [6]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
 RX MEDLINE-20092917; PubMed-10625689;
 RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
 RA Banda M.J.;
 RT "Post-translational proteolytic processing of procollagen C-terminal
 RT proteinase enhancer releases a metalloproteinase inhibitor.";
 RL J. Biol. Chem. 275:1384-1390(2000).
 CC -1- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I
 CC PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
 CC -1- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN
 CC METALLOPROTEINASE INHIBITORY ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 NTR DOMAIN.
 CC -----
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 CC -----
 CC DR EMBL; L37399; AAA61949.1; ALT_SEQ.
 CC DR EMBL; AB008549; BAA23281.1; -;
 CC DR EMBL; AF053356; AAC78800.1; -;
 CC DR EMBL; AF083655; AAD16041.1; -;
 CC DR Gene; HGNC:8738; PCOLCE.
 CC DR MIM; 600270; -;
 CC DR InterPro; IPR000859; CUB_domain.
 CC DR InterPro; IPR001134; Netrin_C.
 CC DR Pfam; PF00431; CUB; 2.
 CC DR Pfam; PF01759; NTR; 1.
 CC DR SMART; SM00042; CUB; 2.
 CC DR PROSITE; PS01180; CUB; 2.
 CC DR Glycoprotein; Repeat; Signal.
 CC FT SIGNAL 1 25 POTENTIAL.
 CC FT CHAIN 26 449 PROCOLLAGEN C-PROTEINASE ENHANCER
 CC FT DOMAIN 37 149 CUB 1.
 CC FT DOMAIN 159 273 CUB 2.
 CC FT SITE 287 288 NTR.
 CC FT SITE 288 289 CLEAVAGE.
 CC FT SITE 293 294 CLEAVAGE.
 CC FT SITE 299 300 CLEAVAGE.
 CC FT SITE 303 304 CLEAVAGE.
 CC FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 449 AA: 47972 MW: 3D88430158648796 CR664;
 Query Match 8.5%; Score 158; DB 1; Length 449;

Best Local Similarity 34.5%; Pred. No. 1.5e-05;
 Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;
 QY 56 GSHSKRFPHPT-IPRMVWLVRLVAVDENVRIQLTDERGLDEDPEDDICKYFVEY--- 111
 Db 168 GLTLTPMPWPSDYPGISCSMHAIAPPDV-IALTE-EKEDLE--PDYCRYSVSFNG 223
 QY 112 EEPSSDSVLGRMCGSGVPKQTSKGNHRIKRVSPDEYFSPGFCIHYSIM----- 164
 Db 224 AVSDDSRRRLKFCGD-AVPSGISSEGNELLVQVPSDLSTVAD-GFSASVKTLPRTAKES 281
 QY 165 --PQVETTSVSPV-LPPSS 180
 Db 282 QCGPKRGTEPEPKVLPKPS 300
 RESULT 12
 NRP2_RAT
 ID NRP2_RAT STANDARD; PRT; 925 AA.
 AC 035276;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropilin-2 precursor (vascular endothelial cell growth factor 165
 DE receptor 2).
 GN NRP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE-97433085; PubMed-9288754;
 RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tal Y.-T., Giger R.J.,
 RA Ginty D.D.;
 RT "Neuropilin is a semaphorin III receptor.";
 RL Cell 90:753-762(1997).
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
 CC AND VEGF-145 ISOMERS OF VEGF. AND THE PLGF-2 ISOMER OF PGF.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
 CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
 CC LINING IN THE RIBS.
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -----
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 CC -----
 CC DR EMBL; AF016297; AAC53338.1; -;
 CC DR HSSP; P12259; ICF2.
 CC DR InterPro; IPR000859; CUB_domain.
 CC DR InterPro; IPR000421; FA58_C.
 CC DR InterPro; IPR000998; MAM_domain.
 CC DR Pfam; PF00431; CUB; 2.
 CC DR Pfam; PF00629; MAM; 1.
 CC DR Pfam; PF00754; F5_F8_Type_C; 2.
 CC DR SMART; SM00042; CUB; 2.
 CC DR SMART; SM00231; FA58C; 2.
 CC DR SMART; SM00137; MAM; 1.
 CC DR PROSITE; PS01180; CUB; 2.
 CC DR PROSITE; PS01285; FA58C_1; 2.
 CC DR PROSITE; PS01286; FA58C_2; 2.
 CC DR PROSITE; PS50060; MAM_2; 1.
 CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
 KW

```

FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 925 NEUROFILIN-2.
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRASMEN 859 883 POTENTIAL.
FT DOMAIN 884 925 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 925 AA; 103896 MM; 3BF62903F644851C CRC64;

Query Match 8.4%; Score 155.5; DB 1; Length 925;
Best Local Similarity 33.3%; Pred. No. 5.7e-05;
Matches 41; Conservative 19; Mismatches 56; Indels 7; Gaps 4;

OY 42 ODRHRHRYTISGNSISHPKPHRYPRNVLMRLVAVDENRQLTFRERGLEPED 101
DB 24 ODPCCGKSKDAGYITSPGYPODIPSHONCEWVYAPPEPNOKIYLVNPHHEIEHD 82
OY 102 DICKEYFVEVEEPDS--VLGRMCGSGYVPGKQTSKGNHRIREFVSEDFEPSEPCIH 159
DB 83 --CKYPIEIRDDSDSADLLGKHGNC-IAPPTIISGSLYIKFTSD-YARGAGGSLR 138
OY 160 YST 162
DB 139 YET 141

RESULT 13
NR22.HUMAN STANDARD; PRT; 931 AA.
ID NR22.HUMAN 014820; 014821;
AC 060462; 014820; 014821;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Neurofilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
DE receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RX SEQUENCE FROM N.A. (ISOFORM A0 AND A17).
RA MEDLINE-97470888; PubMed-9313148;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neurofilin-2, a novel member of the neurofilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III."
RT Neuron 19:547-559(1997).
RN 12
RN SEQUENCE FROM N.A. (ISOFORM A22).
RC TISSUE-Breast;
RX MEDLINE-98188099; PubMed-9529250;
RA Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.;
RT "Neurofilin-1 is expressed by endothelial and tumor cells as an
RT isoform-specific receptor for vascular endothelial growth factor."
RT Cell 92:735-745(1998).
RN 13
RN CHARACTERIZATION.
RP MEDLINE-20309748; PubMed-10748121;

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RA gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neurofilin-2 and neurofilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VEGF) and of placenta
RT growth factor-2, but only neurofilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF."
RL J. Biol. Chem. 275:18040-18045(2000).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3E, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -1- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 AND A17;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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CC -----
CC EMBL: AF022859; AAC51788.1; -
CC EMBL: AF022860; AAC51789.1; -
CC EMBL: AF018098; AAC12922.1; -
CC HSSP: P12259; ICZT.
CC DR Genew: HGNC:8005; NRP2.
CC MIM: 602070; -.
CC DR Interpro: IPR000859; CUB_domain.
CC DR Interpro: IPR000421; FA58_C.
CC DR Interpro: IPR000998; MAM_domain.
CC DR Pfam: PF00431; CUB; 2.
CC DR Pfam: PF00629; MAM; 1.
CC DR Pfam: PF00754; F5_F8_Type_C; 2.
CC DR SMART: SM00042; CUB; 2.
CC DR SMART: SM00231; FA58C; 2.
CC DR SMART: SM00137; MAM; 1.
CC DR PROSITE: PS01180; CUB; 2.
CC DR PROSITE: PS01285; FA58C_1; 2.
CC DR PROSITE: PS01286; FA58C_2; 2.
CC DR PROSITE: PS50060; MAM_2; 1.
CC DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
CC KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 931
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
FT TRASMEN 865 889 POTENTIAL.
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DOMAIN 671 674 POLY-SER.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 839 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 809 813 MISSING (IN ISOFORM A17).
FT VARSPIC 809 830 MISSING (IN ISOFORM A0).
FT CONFLICT 602 602 E -> K (IN REF. 1).
SO SEQUENCE 931 AA; 104830 MM; 270CBAE69A0A97C CRC64;

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ID	VEGF_D RAT	STANDARD;	PRT;	326 AA.
DT	035251;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (Figf).			
GN	FIGF OR VEGFD.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RL	Yamada Y., Hirata Y., Nezu J., Shimane M.;			
RU	submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).			
CC	-1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	-1- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with antiparallel homodimer VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	-----			
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CC	-----			
DR	EMBL; AF014827; AAB66557.1; -			
DR	HSSP; P15692; IVP.			
DR	InterPro; IPR004153; CXXC_repeat.			
DR	InterPro; IPR000072; PD_growth_factor.			
DR	Pfam; PF00341; PDGF_1.			
DR	Pfam; PF03128; CXXC_1.			
DR	ProDom; PD001629; PD_growth_factor; 1.			
DR	SMART; SM00141; PDGF_1.			
DR	PROSITE; PS00249; PDGF_1; 1.			
KW	PROSITE; PS0278; PDGF_2; 1.			
RW	Microgen; Growth factor; Glycoprotein; Signal; Repeat;			
KW	Cleavage on pair of basic residues; Multigene family.			
FT	SIGNAL	1	21	POTENTIAL.
FT	PROPEP	22	93	POTENTIAL.
FT	CHAIN	94	210	VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT	PROPEP	211	326	POTENTIAL.
FT	DOMAIN	227	317	4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
FT				1 (APPROXIMATE).
FT	REPEAT	227	242	2.
FT	REPEAT	263	278	3.
FT	REPEAT	282	298	4. INCOMPLETE).
FT	REPEAT	306	317	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	116	158	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	147	194	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	151	196	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	141	141	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	150	150	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	160	160	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	190	190	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAc. . .) (POTENTIAL).
SO	SEQUENCE	326 AA;	37112 MW;	12616FAJ33596C00 CRC64;

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